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O I O Intelligenetics  
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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-994-064-11.res made by shanley on Fri 27 Sep 102 18:57:03-PDT.

Query sequence being compared: US-09-994-064-11 (1-434)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-994-064-11 (1-434) with:  
File: seq67.pep

```

100- -
N - -
U 50- -
M - -
B - -
E - -
R - -
O - -
F 10- -
S - -
E 5- -
O - -
U - -
E - -
C - -
E - -
S 0- -
SCORE 0 48 96 145 193 241 289 338 386 434
STDEV

```

## PARAMETERS

Similarity matrix Unitary K-tuple  
Mismatch penalty 6 Joining penalty 3  
Gap penalty 5.00 Window size 30  
Gap size penalty 0.33  
Cutoff score 8  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 434 Median 0 Standard Deviation 0.00

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 434  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Init. Opt. Length Score Score Sig. Frame

1. US-09-994-064-67 Sequence 67, Application 434 434 434 0.00 0

1. US-09-994-064-11 (1-434)  
US-09-994-064-67 Sequence 67, Application US/09994064

Initial Score = 434 Optimized Score = 434 Significance = 0.00  
Residue Identity = 100% Matches = 434 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```

X 10 20 30 40 50 60 70
MHRPHLRHSRYAKGEVLTNKHMDGGRCCGAAVFTLFWTCVRIMREHICFVRNAMDRLFLRNAFWTIV
|||||
MHRPHLRHSRYAKGEVLTNKHMDGGRCCGAAVFTLFWTCVRIMREHICFVRNAMDRLFLRNAFWTIV
|||||
X 10 20 30 40 50 60 70

```

```

LSSFPASOSTAAVTDYILGRALDALITPAVGPYNNRLTVSRGCDVLELNPISNDDMTSAKKEKGGP
|||||
LSSFPASOSTAAVTDYILGRALDALITPAVGPYNNRLTVSRGCDVLELNPISNDDMTSAKKEKGGP
|||||
X 80 90 100 110 120 130 140

```

```

FEASVVFYVTKGDGDEKCYPIYRKREYREGCDYQLSECAVQSAQMMADVVPSTLYSRNAGLITFSPFA
|||||
FEASVVFYVTKGDGDEKCYPIYRKREYREGCDYQLSECAVQSAQMMADVVPSTLYSRNAGLITFSPFA
|||||
X 150 160 170 180 190 200 210

```

```

ALSGOYLTLTKIGRPAOTATVLEVNDRCLIGSOLNPLPSKCTTBOYOTGFQGEHLYPADTNTRHADYV
|||||
ALSGOYLTLTKIGRPAOTATVLEVNDRCLIGSOLNPLPSKCTTBOYOTGFQGEHLYPADTNTRHADYV
|||||
X 220 230 240 250 260 270 280

```

```

YRGYEDILORNNNLRRKKNPSAPDPSPVPOEIPAYTKKAEGRTPDAESSEKKAPPEDESDDAQASGEN
|||||
YRGYEDILORNNNLRRKKNPSAPDPSPVPOEIPAYTKKAEGRTPDAESSEKKAPPEDESDDAQASGEN
|||||
X 290 300 310 320 330 340 350 360

```

```

PALPDEDEVEDTEHDDPNSDPDYNDMPAVITVEETTKSSNAVSPITPAFVACAVAGLLVMSIVCA
|||||
PALPDEDEVEDTEHDDPNSDPDYNDMPAVITVEETTKSSNAVSPITPAFVACAVAGLLVMSIVCA
|||||
X 370 380 390 400 410 420 430

```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 2002, 22:36:32 : Search time 2462.5 Seconds  
(without alignments)  
11090.002 Million cell updates/sec

Title: US-09-994-064-10

Sequence: 1 ATGCACCTCTCATCTCAG.....TAAATGCGCGCTAGCTAA 1305

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hgt\_hum:\*  
31: em\_hgt\_inv:\*  
32: em\_hgt\_other:\*  
33: em\_hgtgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Score	Match Length	ID	Description
-----				

1	1305	100.0	1305	6	AR093367	AR093367 Sequence
2	1305	100.0	1305	6	AR135449	AR135449 Sequence
3	1305	100.0	18912	14	ILU28832	U28832 Infectious
4	1268.2	97.2	1627	14	HSWGDGLYCO	L31965 Gallid herp
5	361	27.7	3502	6	A22122	A22122 ILTV gp60 g
6	52.2	4.0	161046	14	AF081810	AF081810 Lymantria
7	45.8	3.5	2676	1	MXARPOD	M32347 M.xanthus s
8	45.8	3.5	7980	1	MXU20669	U20669 Myxococcus
9	44.4	3.4	7218	6	I66494	I66494 Sequence 14
10	43.6	3.3	99360	8	NCB11N2	AL513444 Neurospor
11	43.4	3.3	125020	8	AF429315	AF429315 Homo sapi
12	43	3.3	3022	8	SCYOR053W	274961 S.cerevisia
13	43	3.3	54719	6	SCXV55KB	270678 S.cerevisia
14	41.6	3.2	390	6	AR135147	AR135147 Sequence
15	41.4	3.2	149333	2	AP004592	AP004592 Oryza sat
16	40.4	3.1	195349	2	AC012019	AC012019 Homo sapi
17	40	3.1	12204	1	AE005112	AE005112 Halobacte
18	40	3.1	23407	1	RS024581	AJ245811 Ralstonia
19	40	3.1	30350	8	YSC9315	U10398 Saccharomyc
20	40	3.1	197050	1	AL646081	AL646081 Ralstonia
21	40	3.1	341887	1	AP003006	AP003006 Mesorhizo
22	39.6	3.0	10293	1	AE005012	AE005012 Halobacte
23	39.6	3.0	73476	2	AC101502	AC101502 Mus muscu
24	39.6	3.0	162071	2	AC096932	AC096932 Rattus no
25	39.4	3.0	71517	9	AC073862	AC073862 Homo sapi
26	39.4	3.0	125030	9	AF429315	AF429315 Homo sapi
27	39	3.0	91452	2	AC104273	AC104273 Oryza sat
28	39	3.0	100974	2	AC104715	AC104715 Oryza sat
29	39	3.0	121544	2	AC092779	AC092779 Oryza sat
30	38.8	3.0	489	9	HSTNT5A	X79855 H.sapiens H
31	38.8	3.0	1141	6	AX083744	AX083744 Sequence
32	38.8	3.0	1445	8	SCYIC36	AC007224 Homo sapi
33	38.8	3.0	185327	8	SCYIC36	X04776 Yeast CTC3
34	38.6	3.0	1405	8	SCYIC36	U12980 Saccharomyc
35	38.6	3.0	103682	8	SCYIC36	AC016366 Homo sapi
36	38.6	3.0	163025	2	AC016366	AC005881 cllb_79.e
37	38.6	3.0	181773	9	AC005881	AL137025 Human DNA
38	38.6	3.0	189062	9	AL137025	AL133286 Human DNA
39	38.4	2.9	93354	9	AL133286	AC011154 Homo sapi
40	38.4	2.9	161355	2	AC011154	AC092075 Oryza sat
41	38.4	2.9	164404	2	AC092075	AC019123 Homo sapi
42	38.4	2.9	173016	2	AC019123	L27116 Trypanosoma
43	38.2	2.9	476	3	TRBH1C8AAA	AY051683 Drosophila
44	38.2	2.9	1314	3	AY051683	AC019782 Drosophila
45	38.2	2.9	30278	2	AC019782	

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Score 1305:	DB 6:	Length 1305:
1	AR093367	Sequence 19 from patent US 6001369.	AR093367	AR093367.1	GI:10020117	Unknown.	Unknown.	1 (bases 1 to 1305)	Cochran, M.D. and Junker, D.E.	Recombinant fowlpox viruses and uses thereof	Patent: US 6001369-A 19 14-DEC-1999;	Location/Qualifiers	331 a 349 c 344 g 281 t		100.0%;	100.0%;			

Matches 1305;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	ATGACCGCCCTCATCTCAGACGCGATCGGCTTACTACGGAAAGAGAGAGTGGTTAAC	60					
Db	1	ATGACCGCCCTCATCTCAGACGCGATCGGCTTACTACGGAAAGAGAGAGTGGTTAAC	60					
QY	61	AAACACATGATGCGGTGGAAAGCGGTCTCTCAGCGCAGCTGTATCACTTTTTC	120					
Db	61	AAACACATGATGCGGTGGAAAGCGGTCTCTCAGCGCAGCTGTATCACTTTTTC	120					
QY	121	TGACCTGTGTGATGATTTTGGGGGAGCATCTGCTTGTACGCAAGCTATGACCGC	180					
Db	121	TGACCTGTGTGATGATTTTGGGGGAGCATCTGCTTGTACGCAAGCTATGACCGC	180					
QY	181	CATTATATTTTGAAGAAATGCTTTTGGACTATGCTACTCTTCTTCTCTGCTAGCCAG	240					
Db	181	CATTATATTTTGAAGAAATGCTTTTGGACTATGCTACTCTTCTTCTCTGCTAGCCAG	240					
QY	241	AGCAGCGCGCGCTCAGCTACGACTATTTTAAAGCGCGCTGCGCGCTGACGCGTAAAC	300					
Db	241	AGCAGCGCGCGCTCAGCTACGACTATTTTAAAGCGCGCTGCGCGCTGACGCGTAAAC	300					
QY	301	ATACCGCGGTGGCGCGTAAACAGATACCTCACTAGGGTATCAAGAGGCTGCGAGCTT	360					
Db	301	ATACCGCGGTGGCGCGTAAACAGATACCTCACTAGGGTATCAAGAGGCTGCGAGCTT	360					
QY	361	GTCGAGCTCAACCGATTTTCTAACGTGAGACATATATGCGCGCGCGCAAAAGAAAGAG	420					
Db	361	GTCGAGCTCAACCGATTTTCTAACGTGAGACATATATGCGCGCGCGCAAAAGAAAGAG	420					
QY	421	AAGGGGGGCGCTTTCAGAGCCTCCGTCTGTGTTCTACGTGATTAAGGGCGAGCGCGC	480					
Db	421	AAGGGGGGCGCTTTCAGAGCCTCCGTCTGTGTTCTACGTGATTAAGGGCGAGCGCGC	480					
QY	481	GAGGACAGATCTGTCCATCTATAGAAAGAGATGAGGAAATGAGGCGAGCTACCACTG	540					
Db	481	GAGGACAGATCTGTCCATCTATAGAAAGAGATGAGGAAATGAGGCGAGCTACCACTG	540					
QY	541	CTATCTGAATGCGCGCTTCAATCTGCAAGATGTGGCAGTGAATGTTCTTCTAGCACC	600					
Db	541	CTATCTGAATGCGCGCTTCAATCTGCAAGATGTGGCAGTGAATGTTCTTCTAGCACC	600					
QY	601	CTTGTATCGCAATATGCGCGGAGCTACTATATTTCCCGCAGCTGCGCTCTGCGC	660					
Db	601	CTTGTATCGCAATATGCGCGGAGCTACTATATTTCCCGCAGCTGCGCTCTGCGC	660					
QY	661	CAATCTTGTGACCTCTGAAATCGGAGATTTGGGCAAAAGCTCTGTAACTCTAGAA	720					
Db	661	CAATCTTGTGACCTCTGAAATCGGAGATTTGGGCAAAAGCTCTGTAACTCTAGAA	720					
QY	721	GTTAAGCATCGCTGTTTAAAGATGCGGTGCGACGCTTAACTTTTACCGTCCGAATGCTGG	780					
Db	721	GTTAAGCATCGCTGTTTAAAGATGCGGTGCGACGCTTAACTTTTACCGTCCGAATGCTGG	780					
QY	781	ACAAGAAGAACTATCACTGATTTTCAAGGCGAAACCTTTATCCGATGCGAGACACC	840					
Db	781	ACAAGAAGAACTATCACTGATTTTCAAGGCGAAACCTTTATCCGATGCGAGACACC	840					
QY	841	AATACAGCAGCAGCGAGCATATATCGGAGATACGAAGATTTCTGACGCGCTGGAAT	900					
Db	841	AATACAGCAGCAGCGAGCATATATCGGAGATACGAAGATTTCTGACGCGCTGGAAT	900					
QY	901	AATTTGCTGAGAAAAAAGATCTTAGCGCGCGCAGACCTCTGCTCAGATAGCTCCGCAA	960					
Db	901	AATTTGCTGAGAAAAAAGATCTTAGCGCGCGCAGACCTCTGCTCAGATAGCTCCGCAA	960					
QY	961	GAAATTCGCGCTGTACCAAGAAAGCGGAGGCGCACCCCGAGCGCAAGAAAGCGAGAA	1020					
Db	961	GAAATTCGCGCTGTACCAAGAAAGCGGAGGCGCACCCCGAGCGCAAGAAAGCGAGAA	1020					
QY	1021	AAGAAGCGCCCTCAGAGACTGCGAGGAGCAGATGCAAGAGGCTTCTGAGAAAAAT	1080					
Db	1021	AAGAAGCGCCCTCAGAGACTGCGAGGAGCAGATGCAAGAGGCTTCTGAGAAAAAT	1080					

QY	1081	CTGCGCGCCCTCCCGAGACGAGAAAGTCCCGAGACACCGAGACGATGATCCAAAC	1140					
Db	1081	CTGCGCGCCCTCCCGAGAGCGAAGTCCCGAGACACCGAGACGATGATCCAAAC	1140					
QY	1141	TGCGATCTGACTATTTACATGACATGCGCGCGGTGATCCGGTGGAGAGACTACTAA	1200					
Db	1141	TGCGATCTGACTATTTACATGACATGCGCGCGGTGATCCGGTGGAGAGACTACTAA	1200					
QY	1201	AGTTCTAATGCGCTCCATGACCCATATTCGCGCGGTGCTAGACCTGCGCGGTCTC	1260					
Db	1201	AGTTCTAATGCGCTCCATGACCCATATTCGCGCGGTGCTAGACCTGCGCGGTCTC	1260					
QY	1261	GTCGAGCTACTGTTTGGAGCATGCTAAATGGCGCGGTAGCTAA	1305					
Db	1261	GTCGAGCTACTGTTTGGAGCATGCTAAATGGCGCGGTAGCTAA	1305					
RESULT	2							
ARI35449		ARI35449	1305 bp	DNA	linear	PAT	16-JUN-2001	
LOCUS		Sequence	19	from patent	US 6136318			
DEFINITION		ARI35449						
ACCESSION		ARI35449						
VERSION		ARI35449.1	GI:14476121					
KEYWORDS		Unknown.						
SOURCE		Unknown.						
ORGANISM		Unclassified.						
REFERENCE		1 (bases 1 to 1305)						
AUTHORS		Cochran, M.D. and Junker, D.E.						
TITLE		Recombinant fowlpox viruses and uses thereof						
JOURNAL		Patent: US 6136318-A 19 24-OCT-2000;						
FEATURES		location/Qualifiers						
source		1. 1305						
BASE COUNT		331 a 349 c 344 g 281 t						
ORIGIN								
Query Match		100.0%; Score 1305; DB 6; Length 1305;						
Best Local Similarity		100.0%; Pred. No. 0;						
Matches 1305; Conservative		0; Mismatches						
QY	1	ATGACCGCTCTCATCTCAGACGCGATCGGCTTACTACGGAAAGAGAGAGTGGTTAAC	60					
Db	1	ATGACCGCTCTCATCTCAGACGCGATCGGCTTACTACGGAAAGAGAGAGTGGTTAAC	60					
QY	61	AAACACATGATGCGGTGGAAAGCGGTCTCTCAGGCGCAGCTGTATTCACCTTTTC	120					
Db	61	AAACACATGATGCGGTGGAAAGCGGTCTCTCAGGCGCAGCTGTATTCACCTTTTC	120					
QY	121	TGACCTGTGTGATGATTTTGGGGGAGCATCTGCTTGTACGCAAGCTATGACCGC	180					
Db	121	TGACCTGTGTGATGATTTTGGGGGAGCATCTGCTTGTACGCAAGCTATGACCGC	180					
QY	181	CATTATATTTTGAAGAAATGCTTTTGGACTATGCTACTCTTCTTCTCTGCTAGCCAG	240					
Db	181	CATTATATTTTGAAGAAATGCTTTTGGACTATGCTACTCTTCTTCTCTGCTAGCCAG	240					
QY	241	AGCAGCGCGCGCTCAGCTACGACTACATTTTAAAGCGCGCTGCGCGCTGACGCGCTAAC	300					
Db	241	AGCAGCGCGCGCTCAGCTACGACTACATTTTAAAGCGCGCTGCGCGCTGACGCGCTAAC	300					
QY	301	ATACCGCGGTGGCGCGTATTAACATATACCTCACTAGGGTATCAAGAGGCTGCGAGCTT	360					
Db	301	ATACCGCGGTGGCGCGTATTAACATATACCTCACTAGGGTATCAAGAGGCTGCGAGCTT	360					
QY	361	GTCGAGCTCAACCGATTTTCTAACGTGAGACATATATGCGCGCGCAAAAGAAAGAG	420					
Db	361	GTCGAGCTCAACCGATTTTCTAACGTGAGACATATATGCGCGCGCAAAAGAAAGAG	420					
QY	421	AAGGGGGGCGCTTTCAGAGCCTCCGTCTGTGTTCTACGTGATTAAGGGCGAGCGCGC	480					
Db	421	AAGGGGGGCGCTTTCAGAGCCTCCGTCTGTGTTCTACGTGATTAAGGGCGAGCGCGC	480					



Db 421 AAGGGGGCCCTTTCGAGCCCTCCGCTGCTGTTCTACGTATTAAGGGCGAGCAGCGC 480  
Qy 481 GAGGACAGTACGTCCAACTCTATAGAAAGAGTACAGGAATGTGGCAGCTCACTG 540  
Db 481 GAGGACAGTACGTCCAACTCTATAGAAAGAGTACAGGAATGTGGCAGCTCACTG 540  
Qy 541 CTATCTGAATGCGCGCTTCATCTGCACAGATGGGACGTGACATGTTTCTCAGACC 600  
Db 541 CTATCTGAATGCGCGCTTCATCTGCACAGATGGGACGTGACATGTTTCTCAGACC 600  
Qy 601 CTGTATCGGGAATGGCGGGGAGCTGACATATATTTCCCCACTGCTGCGCTCTGGC 660  
Db 601 CTGTATCGGGAATGGCGGGGAGCTGACATATATTTCCCCACTGCTGCGCTCTGGC 660  
Qy 661 CAATACTGCTGACCCGGAATTCGGAGATTTGGCGAAACAGCTCTCCTAGTGA 720  
Db 661 CAATACTGCTGACCCGGAATTCGGAGATTTGGCGAAACAGCTCTCCTAGTGA 720  
Qy 721 GTTACGATCGCTGTTTAAAGATCGGGTCCAGCTTAACTTTTAACTCGAATGCTGG 780  
Db 721 GTTACGATCGCTGTTTAAAGATCGGGTCCAGCTTAACTTTTAACTCGAATGCTGG 780  
Qy 781 ACAACAGAACGATATGACATGATTTCAAGGCGAACACCTTATCCGATCGCAGACCC 840  
Db 781 ACAACAGAACGATATGACATGATTTCAAGGCGAACACCTTATCCGATCGCAGACCC 840  
Qy 841 AATACACGACACCGCGGACGCTATATCGGGGATACGAATATTTCTGACGCGTGGAA 900  
Db 841 AATACACGACACCGCGGACGCTATATCGGGGATACGAATATTTCTGACGCGTGGAA 900  
Qy 901 AATTTGCTGGAAGAAAGATTCAGCGGCGCAGACCTGCTCAGATGATGCTCCGCAA 960  
Db 901 AATTTGCTGGAAGAAAGATTCAGCGGCGCAGACCTGCTCAGATGATGCTCCGCAA 960  
Qy 961 GAATTTCCCGCTGTAACCAAGAAAGCGGGAAGGGCGCACCCCGGACGAGAAAGCAGCAA 1020  
Db 961 GAATTTCCCGCTGTAACCAAGAAAGCGGGAAGGGCGCACCCCGGACGAGAAAGCAGCAA 1020  
Qy 1021 AAGAAGGCCCCCTCAGAAAGCTCGGAGGACGACATGCGACAGAGCTTCTGAGAAAT 1080  
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Qy 1081 CCGGCGGCCCCCTCCCGGAGAGCAAGATCCCGGAGGACGACGAGCATGATCCCAAC 1140  
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Qy 1201 AGTTCTTAATCCGCTCTCCATATTTGGCGCGTTCGTAGCTGCGCGCTGCGCTC 1260  
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Qy 1261 GTGGGGTACTGGTTTGAGCATGTAATATGGCGGTAGCTAA 1305  
Db 1261 GTGGGGTACTGGTTTGAGCATGTAATATGGCGGTAGCTAA 1305

RESULT 3  
ILU28832 18912 bp DNA linear VRL 09-AUG-1996  
LOCUS ILU28832  
DEFINITION Infectious laryngotracheitis virus US10, US2, protein kinase, UL47,  
glycoprotein G, ORF5, glycoprotein D, glycoprotein I, glycoprotein  
E, ORF9 genes, complete cds.  
ACCESSION U28832  
VERSION U28832.1  
KEYWORDS GI:1486484  
SOURCE Infectious laryngotracheitis virus.  
ORGANISM Gallid herpesvirus 1  
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;  
Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.  
REFERENCE 1 (bases 1 to 18912)

AUTHORS Wild, M.A., Cook, S. and Cochran, M.  
TITLE A genomic map of infectious laryngotracheitis virus and the  
sequence and organization of genes present in the unique short and  
flanking regions  
JOURNAL Virus Genes 12 (2), 107-116 (1996)  
MEDLINE 97033380  
REFERENCE 2 (bases 1 to 18912)  
AUTHORS Wild, M.A.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUN-1995) Martha A. Wild, Syntro Research Laboratory,  
3535 General Atomics Court, San Diego, CA 92121, USA  
FEATURES  
source  
1. 18912  
/organism="Gallid herpesvirus 1"  
/strain="USDA challenge strain"  
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/rpt\_type="inverted  
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QSENMRFVLEKELSLWSRLPADLSAHERTSRLSAGHMCCLMHPRCRACLYD  
SIVOSLFCVGTGRVPQSEMRREVIYLAALRAGAAANSPEVSASIFARDAGIALALR  
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GPDILSFSAVLEPLVLYIRARGASRSRHHNQSAPAAGLAALRIEMEVRSLLV  
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2910..16003  
/note="short unique region"  
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RPSLTVIAKPAVLEVSSELESLPRKCRVIRFEGGSDPGVSPWMSGDLGAKTMSYD  
SGAVAAKEHLWLWLTADICMALNIPARVFLITETGKNFREGVLEILVNDKTLT  
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SKKPRSPRRRR"  
3694..5124  
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 VERSION U31965.1 GI:493595  
 KEYWORDS glycoprotein D,  
 SOURCE Gallid herpesvirus 1.  
 ORGANISM Gallid herpesvirus 1  
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

REFERENCE 1 (bases 1 to 1627)  
 AUTHORS Johnson,M.A., Tyack,S.G., Pridoux,C.T., Kongsuwan,K. and Sheppard,M.  
 TITLE Sequence characteristics of a gene in infectious laryngotracheitis virus homologous to glycoprotein D of herpes simplex virus  
 JOURNAL DNA Seq. 5 (3), 191-194 (1995)  
 MEDLINE 95337426  
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 Db 155 ATGACCGTCTCATGTCACAGGCACTGCGCTTACTACGCGAAGAGAGGCTTAAAC 214  
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KEYWORDS  
SOURCE Myxococcus xanthus.  
ORGANISM Bacteria; Proteobacteria; delta subdivision; Myxobacteria;  
REFERENCE Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.  
AUTHORS 1 (bases 4593 to 7280)  
TITLE Cloning and DNA sequence of the gene coding for the major sigma  
factor from Myxococcus xanthus  
JOURNAL J. Bacteriol. 172 (1), 80-85 (1990)  
MEDLINE 90094274  
REFERENCE 2 (bases 1 to 7980)  
AUTHORS Davis, J.M., Mayor, J. and Plamann, L.  
TITLE A missense mutation in rpoD results in an A-signalling defect in  
Myxococcus xanthus  
JOURNAL Mol. Microbiol. 18 (5), 943-952 (1995)  
MEDLINE 96422481  
REFERENCE 3 (bases 1 to 7980)  
AUTHORS Plamann, L.S.  
TITLE Direct Substitution  
Submitted (06-FEB-1995) Lynda S Plamann, Department of Biology,  
Texas A & M University, College Station, TX 77843-3258, USA  
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JOURNAL	Eukaryota: Fungi; Ascomycota: Pezizomycotina; Sordariomycetes:					
REFERENCE	Sordariales: Sordariaceae; Neurospora.					
AUTHORS	1 (sites)					
JOURNAL	Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Partmann,B.,					
REFERENCE	Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G..					
AUTHORS	2 (bases 1 to 99360)					
TITLE	German Neurospora genome/project.					
JOURNAL	Direct Submission					
COMMENT	Submitted (08-NOV-2001) MIPS, Institut fuer Bioinformatik, GSP-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, E-mail: ulrich.schulte@uni-duesseldorf.de Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, <a href="http://www.mwgda.com">http://www.mwgda.com</a> this contig is an assembly of BAC BLIN2 from 1 to: 91660, strain ORF4A, and cosmid 65g7 from 91661 to: 99360, cosmid library PLORIST6kh, strain 74-OR-23-JA; BAC and cosmid clones are available at the Fungal Genetic Stock Center, <a href="http://www.fgsc.net">http://www.fgsc.net</a> Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: <a href="http://mips.gsf.de/proj/neurospora">http://mips.gsf.de/proj/neurospora</a> .					
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ACCESSION AF429315  
VERSION AF429315.1 GI:17646244  
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REFERENCE  
1 (bases 1 to 125020)  
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.  
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2  
Nat. Genet. 29 (4), 377-378 (2001)  
JOURNAL  
MEDLINE 21583737  
PUBMED 11694876  
REFERENCE 2 (bases 1 to 125020)  
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.  
Direct Submission  
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA  
JOURNAL  
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REFERENCE  
1 (bases 1 to 616)  
Landt,O., Hiesel,R. and Unsel,J.M.  
JOURNAL  
AUTHORS Unpublished  
REFERENCE 2 (bases 1 to 3022)  
Bohn,C., Bolotin-Fukuhara,M., Daignan-Fornier,B., Dang,D.V. and Valens,M.  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 3022)  
AUTHORS MIPS.  
TITLE Direct Submission



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Scoring table: IDENTITY\_NUC  
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Searched: 1736436 seqs, 858457221 residues

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12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1305	100.0	1305	15	AAQ68944
2	1305	100.0	1305	15	AAQ68944
3	1305	100.0	1305	20	AAQ68944
4	1305	100.0	1305	21	AAQ68944
5	1305	100.0	1305	21	AAQ68944
6	1305	100.0	1305	21	AAQ68944
7	1305	100.0	1305	21	AAQ68944
8	1305	100.0	1305	21	AAQ68944
9	1305	100.0	1305	21	AAQ68944

10	42	3.2	42	17	AAQ4399
11	41.6	3.2	390	13	AAQ21833
12	41.6	3.2	390	14	AAQ36859
13	41.6	3.2	390	22	AAQ76910
14	38.4	2.9	1761	21	AAQ44461
15	38.2	2.9	1232	23	ABLI1609
16	38.2	2.9	3038	23	ABLI16776
17	38.2	2.9	3232	23	ABLI1608
18	37.4	2.9	2277	19	AAV13834
19	37.4	2.9	2277	19	AAV05370
20	36.8	2.8	1450	12	AAQ13227
21	36.8	2.8	1450	12	AAQ13408
22	36.8	2.8	3395	21	AAQ00601
23	36.2	2.8	2943	17	AAQ16480
24	35.6	2.7	429	20	AAQ27978
25	35.6	2.7	429	20	AAQ66005
26	35.6	2.7	810	23	ABLI14835
27	35.6	2.7	1680	23	AAQ68538
28	35.6	2.7	2428	22	AAQ29596
29	35.6	2.7	3642	21	AAQ96040
30	35.6	2.7	4091	21	AAQ50603
31	35.6	2.7	4422	21	AAQ87685
32	35.6	2.7	5610	20	AAQ28008
33	35.6	2.7	5610	21	AAQ96035
34	35.6	2.7	5610	21	AAQ96041
35	35.6	2.7	5659	21	AAQ87686
36	35.4	2.7	1364	14	AAQ35092
37	35.4	2.7	3489	21	AAQ30280
38	35.4	2.7	3489	22	AAQ82901
39	35.4	2.7	32207	19	AAQ73805
40	35.4	2.7	137507	19	AAQ19941
41	35.2	2.7	150	20	AAQ64956
42	35.2	2.7	625	21	AAQ45074
43	35.2	2.7	707	24	ABLI1484
44	35.2	2.7	1508	21	AAQ43746
45	34.6	2.7	1194	21	AAQ51529

#### ALIGNMENTS

RESULT	ID	AAQ68944 standard; DNA: 1305 BP.
AC	AAQ68944:	
DT	13-APR-1995 (first entry)	
DE	gd gene of infectious laryngotracheitis virus (ILT).	
XX		
XX	Homology vector 586-36.6; gd gene; cassette gene; ss.	
OS	Infectious laryngotracheitis virus.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..1305
XX		/tag- a
PN	MO9419014-A.	
PD	01-SEP-1994.	
XX		
PF	28-FEB-1994.	94MO-US01826.
XX		
PR	26-FEB-1993.	93US-0024156.
XX		
PA	(JAPC) NIPPON ZEON KK.	
XX	(SYTR) SYNTRON CORP.	
PI	Cochran MD;	
XX		
DR	WPI: 1994-294007/36.	

Homology vector 56  
Randomising oligon  
PCR primer for 5'  
Sequence containin  
Zea mays DNA fragm  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Homo sapiens ambig  
Human telomerase p  
PRV glycoprotein g  
Pseudorabies virus  
Human membrane tra  
SAB virus gb glyco  
Human leccomedin-1  
Human leccomedin-1  
Drosophila melanog  
DNA encoding novel  
Human endocrine po  
Human leccomedin-2  
Human leccomedin-2  
Human G protein-co  
Human leccomedin-2  
Originally determi  
Resequenced human  
Grass pollen aller  
Kapsid s sarcoma-a  
Nucleotide sequenc  
KSHV LTR DNA (nucl  
KSHV long unique c  
Mouse histone H2B  
Archidopsis thalia  
Murine apoptosis r  
Zea mays DNA fragm  
S. paucimobilis am

DR P-PSDB; AAR58856.  
 XX  
 PT New recombinant fowl pox virus for use in vaccines - contains  
 PT genes expressing antigens of Newcastle disease virus and opt.  
 PT Infectious bronchitis virus  
 XX  
 PS Disclosure; Page 74-75; 85pp; English.  
 XX  
 CC AA06944 contains the coding region of the ILT gd gene and was  
 CC derived from an approx. 2060 bp EcoRI to BclI restriction sub-  
 CC fragment of the ILT KpnI genomic restriction fragment #8 (10.6kb).  
 CC It is part of a cassette in plasmid 586-36.6 constructed for  
 CC the purpose of inserting ILT gb and gd genes into the fowlpox  
 CC virus (FPV).  
 XX  
 XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 1305; DB 15; Length 1305;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCTCATCTGAGACGCGACCTGGTTACTACGGGAAAGAGAGCTCTTAAAC 60  
 Db 1 atgcacgcctccatccatcagacgcgcgtctactacggaagagagtgcttaac 60  
 QY 61 AAACACATGATGGGTGGGAAAAAGGTGCTCAGCGCGACCTGATTCACCTCTTTC 120  
 Db 61 aaacacatgagatcgcgtggaagaggtgctcagcgagcgagctgtattcacctcttc 120  
 QY 121 TGGACTTGTCAGATATTGCGGAGCATATCTGCTTGTGACCAACGCTATGAGACGC 180  
 Db 121 tggacttgcagagatattgcggaagacatactgcttgcagcaacgctatgagacgc 180  
 QY 181 CATTATTTTGGAGATNGCTTTTGGACTATGCTACTGCTTCTTCCTTGGCTAGCCAG 240  
 Db 181 cattatttggagaaatgcttcttggactactgctactgcttcttcccttcgtagccag 240  
 QY 241 AGCAGCGCGCGCTCAGTACGACTATTTAGCGCGTGGCGGCTCAGCGGCTAACCC 300  
 Db 241 agcagcgcgcgctcagctacgactaatcttggcgctgcgcgtcagcgctaaccc 300  
 QY 301 ATTCCGGCGGTGGCCCGTATTAACAGATACCTAGGATATCAAGAGCGTGCAGCTT 360  
 Db 301 ataccggcggttggcccgatatacaagatacctcactcaggatcagagcgctgagctt 360  
 QY 361 GTCGAGCTCAACCGATTCTTACGTGAGACATGATATTCGGCGGCCAAAAGAGAG 420  
 Db 361 gtcgagctcaacccgatttcttaacgtgagacatgatactgcgcgccaagaaagag 420  
 QY 421 AAGGGGGGCCCTTTCGAGGCTCCGCTGCTGTTCTACGATTAAAGGCGACGAGGC 480  
 Db 421 aaggggggccccttcgagggcctcgcgtgctgttctacgattaaaggcgagcgagc 480  
 QY 481 GAGGACATGATGTCATCTATAGAAAGAGTACAGGAATGCGGAGCTACACTG 540  
 Db 481 gaggaacagtaactgtccaatctatagaagagtaagagatgagagctacactg 540  
 QY 541 CTATCTGAATGGCGCGTTCATCTGCACAGATGTGGGAGTGAATGATCTAGACCC 600  
 Db 541 ctatctgaatggcgcttcaatctgcacagatgtgggagtgagactatgttccagacc 600  
 QY 601 CTGTATGCGCAATGGGCGGAGCTGACTATATTCCTCCCACTGCTGCGCTCTGCG 660  
 Db 601 ctgtatcgcaaatggcgggagctgactatattctcccaactgctgcgtctcgcg 660  
 QY 661 CAATACTTGTGACCTGGAATCGGAGATTTGCGCAACAGCTGCGTAACCTAGAA 720  
 Db 661 caatactgtgcacccggaatcgagagatttgcgaacagcttcgtaactagaa 720  
 QY 721 GTTAACGATGCGCTTTTAAAGATGGGTGCGAGCTTAACTTTTACCGTGAATGCTG 780  
 Db 721 gttaacgatgcgtttttaaagatgggtgcgagctttaaacttttacgcgtgaatgctg 780

QY 781 ACACAGACAGATTCAGACTGGATTTCAGGGCAACACCTTATCCATCCAGACACC 840  
 Db 781 acaacagacagatctcagactggatttcagggcaaacaccttattccgtcgcagacac 840  
 QY 841 AATACAGACAGCGGAGCGAGTATATCGGGGATATGAGATATTTGACGCGTGAAT 900  
 Db 841 aatacagacagcgagcgagctatctcggggatacgaagatattctgcagcgctgaat 900  
 QY 901 AATTTGCTGAGAAAAAGAAATCCTAGCGGCCAGACCTCTGTCAGATAGCTCCGCA 960  
 Db 901 aatttgcctgagaaaaagaaatcctlagcgcgcaagacctctgcagataagctccgca 960  
 QY 961 GAATTCGCCGTGTACCAAGAAAGCGAAGCGCCGACCCCGACGCAAGAAACAGCGAA 1020  
 Db 961 gaattccgcgtgtaccaaagaaagcgaaagcgaccccgacagcagaagacgaa 1020  
 QY 1021 AAGAGGCCCCCTCCAGAAACCTCGAGACGACATGACGAGCGAGGCTTGGGAAAT 1080  
 Db 1021 aagaagccccctccagaaacctcgagacgacatgacgagcgagagcttcggaagaa 1080  
 QY 1081 CCTGCCGCCCTCCCGAAGACGACGAAGTCCCGGAGACACCGACAGATGATCAAC 1140  
 Db 1081 cctgcgcgcctcccgaaagacgaagctcccgagacaccgagcaagatgaccaac 1140  
 QY 1141 TCGGATCTGACTATTACAAATGACATGCCCGCGGATCCCGGTGAGAGACTATAA 1200  
 Db 1141 tcggatctgactattacaaatgacatgcccgcggtatcccggtgagagactataa 1200  
 QY 1201 AGTTAATGCGGCTTCATGATCCCATATTCGCGGCTTGTGAGCTTCGCGGCTC 1260  
 Db 1201 agttaatgcggcttcattgatcccatatttcgcggttgtgagcttcgcggtcgc 1260  
 QY 1261 GTGGGCTACTGCTTGGAGCATGTAAATGCGCGGTAGCTAA 1305  
 Db 1261 gtgggctactgcttggagcatgtaaatgcgcggtagcttaa 1305

RESULT 2  
 AAT33505  
 ID AAT33505 standard; DNA: 1305 BP.

AC AAT33505;  
 DT 19-NOV-1996 (first entry)  
 XX

DE Infectious laryngotracheitis virus gd gene.

KW Infectious laryngotracheitis virus; ILTV; herpesvirus;  
 KW attenuation; vector; vaccine; chicken; poultry; immunisation;  
 KW glycoprotein gp; ds.

OS Infectious laryngotracheitis virus.

XX  
 PN WO9508622-A1.

XX 30-MAR-1995.

XX 16-SEP-1994; 94WO-US10628.

XX 24-SEP-1993; 93US-0126597.

XX (SYNR ) SYNTRO CORP.

XX Cochran MD, Wild MA;

XX WPI, 1995-139591/18.

XX P-PSDB; AAW00638.

PT Recombinant attenuated infectious laryngotracheitis virus - for use  
 PT in vaccines to protect poultry from infection from the virus; also  
 PT methods of distinguishing between vaccinated and naturally infected  
 PT birds



XX Example 1: Page 106-107; 177pp; English.

CC The gp gene (AAT33505) spans bases 8462-9766 of the unique short  
CC region (see also AAT33504) of infectious laryngotracheitis virus  
CC (ILT) genomic DNA. It codes for a glycoprotein (AAM00638) of  
CC approx. 48,477 mol. wt. that is homologous to pseudorabies  
CC virus 950 and to gp from herpes simplex virus-1, Marek's  
CC disease virus, IPV and bovine herpesvirus-1.1. Monoclonal  
CC antibodies raised to ILTV react specifically with gp from  
CC ILTV and also with ILTV gp expressed in herpesvirus of  
CC turkeys (HVT) virus vector. ILTV gp expressed in the HVT  
CC vector is useful as a subunit vaccine.

XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 16; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACCGTCCTCATCTCAAGACGGCTCGGTTACTACGGGAAAGAGAGTGTAAAC 60  
DB 1 atgcaccgctccatccacagcgcactcgcttactacggaagagagtgcttaac 60  
QY 61 AACACATGATGGGTTGGGTAAGAAAGGCTGCTCAGCGGAGCTGATTCACCTTTTC 120  
DB 61 aaacacatgatgggttggaagaaagcgtgctcagcgcaagctgtaactctcttc 120  
QY 121 TGCACCTGTGTCAAGATTATGCGGACATATGCTTTGACGCAACGCTATGACGCG 180  
DB 121 tgcacctgtgtcaagattatgcggacatattgctttgacgcaacgctatgacgcg 180  
QY 181 CATTATTTTGAAGAAATGCTTTTGGACATATGCTACTGCTTCTCTTCGCTAGCCAG 240  
DB 181 cattattttgaaagaaatgcttttggacatattgctactgcttctcttccttcgtagccag 240  
QY 241 AGCACCCCGCCCGTCACGTAAGACTATTTAGCCGCTGCGGCGTCGACGCCCTAAC 300  
DB 241 agcaccccgcccgctcacgtaagactattttagccgctgcgcgctcgcagcgttaac 300  
QY 301 ATACCGGCGGTTGGCCGTATACAGATACCTCACTAGGATACAGAGGCTGCGAGCTT 360  
DB 301 ataccggcggttgccggtataacagatactcaactagggtataaagagtgcgagctt 360  
QY 361 GTGAGCTCAACCGATTTCTAACGTGACACATGATATCGGCGCCAAAGAAAAGAG 420  
DB 361 gtgagctcaacccgattcttaacgtgacacatgatactcgcgccaaagaaaagag 420  
QY 421 AAGGGGGCCCTTTCCAGGCGCTCGCTGCTGCTTCTACGTTAAGGGCGACGAGCGC 480  
DB 421 aagggggccctttccaggcgctcgcgtcgtctgcttacgtaagggcgagagagc 480  
QY 481 GAGGACAGTACTGTCATCTATAGAAAAGATGACGAGGAAATGGCGAGCTGCAACTG 540  
DB 481 gaggacagtactgtcattctatagaaaagatgacgaggaatggcgagctgcaactg 540  
QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTGGCAGTGAATGTTCTTCTACGACC 600  
DB 541 ctatctgaatgcgcgcttcaatctgacagatgtggcagtgaactgtctccagacc 600  
QY 601 CTGTGATCGGAAATGGCGGGGACGACTGATATTTCTCCCGCACTGCTGGCTCTGCGC 660  
DB 601 ctgtgatcggaatggcggggacgactgatatcttcccccactgtcgcctctgyc 660  
QY 661 CAATACCTGTGACCCGGAATTCGGAGATTTGGCAACAGCTCTCGTAACCTAGAA 720  
DB 661 caatacctgtgacccggaaatfcggagatttggcgaacagctctcgtaacctagaa 720  
QY 721 GTTAACGATCGCTGTTTAAAGATCGGGTCGACGTTAACTTTTACCGTGAAATGCTGG 780  
DB 721 gttaacgatcgctgtttaaagatcgggctcgacgtttaaacttttacccgtgaaatgctgg 780

QY 781 ACAACAGACAGTATACAGCTGATTTCAAGCGCAACACCTTTATCCGATCGACAGCC 840  
DB 781 acaacagacagatatacagctgatttcaagcgcaacacctttatccgatcgacagacc 840  
QY 841 AATACAGACAGCGGAGCAGCTATATCGGGATACGAAGATATTCGACGCTGGAAT 900  
DB 841 aatacagacagcgagacgactatctcgggatacgaagatattctcgcagcgttgaa 900  
QY 901 AATTGCTGAGGAAAAGATTCCTAAGCGCGCCAGACCTCTCTCCAGATAGCTCCGCA 960  
DB 901 aattgctgagggaaaagattcctaagcgcgccagacctctctcagataagcgtccgaa 960  
QY 961 GAAATTCGCGCTGTACCAAGAAAGCGGAAGGCGCACCCCGGACGCAAGAAAGCGCAA 1020  
DB 961 gaaatfcgctgtaaccaagaagcggaagcgcaaccggacggcagagaagcagcga 1020  
QY 1021 AAGAAGCCCTCCAGAAAGTCTGAGAGACGACATGACGAGCAGAGCTTCTGGAATAAT 1080  
DB 1021 aagaagccctccagaagactcgagagacatagcagagagcgtctcgagaaat 1080  
QY 1081 CCTCCGCGCTCCCGGAAGACGAGAAAGTCCCGAGACACCGACGATGATCAAAAC 1140  
DB 1081 cctccgcgctcccggaagacgaaagtcctcgagagacacgagacgataccaaac 1140  
QY 1141 TCGGATCCTGACTATTAACAATGACATGCGCGCGTGATCCCGTGGAGAGACTATAA 1200  
DB 1141 tcggatcctgactatttaacaatgacatgcccgcgtgatcccggtggagagactataa 1200  
QY 1201 AGTTCTAATGCGGCTCTCCATGCCATATTCGCGGCGTTGATGAGCTCGCGGTGCGCTC 1260  
DB 1201 agttctaattgcggtctccatgccatatttcgcgcggttgatgagctcgtcggtcgc 1260  
QY 1261 GTGGGCGTACTGTTTGGAGCATGTAAATGCGCGCGTACTAA 1305  
DB 1261 gtgggctactggttggagcatgtaaatgcgcgcgtaactaa 1305

# RESULT 3

AAH8152 standard; DNA: 1305 BP.

AAH81152:

07-SEP-1999 (first entry)

Seq ID No: 19 of US925358.

Fowlpox virus; FPV, recombinant; vaccine; immunisation; chicken; NDV.

Newcastle disease virus; NDV, Fowlpox; Infectious laryngotracheitis; ds.

Fowlpox virus.

US925358-A.

20-JUL-1999.

07-JUN-1995; 95US-0484575.

07-JUN-1995; 95US-0484575.

26-FEB-1993; 93US-0024156.

28-FEB-1994; 94WO-US02252.

(SYTR ) SYNTRO CORP.

Cochran MD, Junker DE;

WPI: 1999-418249/35.

P-PADB; AAT21984.

Fowlpox viruses, useful as vaccines for immunization of

PT chickens/turkeys against Fowlpox and Newcastle disease virus

XX Disclosure; Columns 77-82; 108pp; English.

XX The invention relates to a recombinant fowlpox virus (FPV) comprising  
 CC a foreign DNA inserted into a region of the fowlpox virus genome  
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a  
 CC host cell. The virus is used as a vaccine for immunising chickens against  
 CC Newcastle disease virus (NDV), Fowlpox, and infectious laryngotracheitis.  
 XX Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match 100.0%; Score 1305; DB 20; Length 1305;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACCGCTCTCATCTCAGACGACCTGCTTACTACGGAAGAGAGTGGTTTAC 60  
 Db 1 atgcaccgctccatctcagacgacctcgttactacgcaaaagagagtgcttaac 60  
 QY 61 AACACATGAGATTGGGGTGGAAAACGCTGCTCAGCGCAGCTGTATTCATCTTTTC 120  
 Db 61 aaacacatgagattgggggtggaaaacgctgctcagcgagcgtgtattcattcttcc 120  
 QY 121 TGGACTTGTGAGATTATGCGGAGCATATGCTTTGTAGACGACGATATGACCCG 180  
 Db 121 tggacttgtagattatgctggagcatatgctttgttagacgacgacgtatgacccg 180  
 QY 181 CATTTATTTTGGAGAAATGCTTTTGGACTATGCTACTGCTTCTTCTTCTGCTAGCCAG 240  
 Db 181 catttattttggagaaatgcttttggactatgctactgaggtatccttctctgtagccag 240  
 QY 241 AGACACCGCGCGCTACGCTACGACTACATTTTAGCGCTGCGGCGCTGACGCGCTAAC 300  
 Db 241 agacaccgcgcgctacgctacgactacatTTTAGCGCTGCGGCGCTGACGCGCTAAC 300  
 QY 301 ATACCGGGGTTGGCCGCTATTAACAGATACCTCACTAGGGATCAAGAGGCTGCGACGTT 360  
 Db 301 ataccggggttggcccgctatttaacagatacctcaactagggatcaagaggctgcgacgt 360  
 QY 361 GTGAGCTCAACCGGATTTTCAAGTGGAGACAGATGATATGCGGCGCAAGAAAAGAG 420  
 Db 361 gtgagctcaaccggatTTTCAAGTGGAGACAGATGATATGCGGCGCAAGAAAAGAG 420  
 QY 421 AAGGGGGCCCTTTCAAGGCGCTCCGCTGCTGCTTACGATTAAGGGCGAGCGCGC 480  
 Db 421 aagggggcccctttcaaggcgctccgctgcttacctgagtttaaggcgagcgcgcc 480  
 QY 481 GAGGACAGTACGTTCCATCTATAGAAAAGACTACAGGAATGTGGCGACTGTAACCTG 540  
 Db 481 gaggacaagtacgttccatctatagaaaagactacaggaatgtggcgactgttaacctg 540  
 QY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGTTGGGAGTGGAGTATGTTCTTACAC 600  
 Db 541 ctatctgaatgcgcgcttcaatctgacagatgtgggagtggaactatgttctttagcac 600  
 QY 601 CTTGTATCGGAAATGGCGGGGACTGACTATATTTCTCCCACTGCTCGCTCTGAGC 660  
 Db 601 ctgtatcggaatggcggggactgactatatttctcccaactgctcgcctctctggc 660  
 QY 661 CAATACTTGTGACCTCGGAAATCGGAGATTTGGCAACAGCTCTGTAACCTAGAA 720  
 Db 661 caatacttgtgacctcggaatcggaatctgcaaaagcctctgtaaccttagaa 720  
 QY 721 GTTAAAGATCGCTTTAAAGATCGGAGTTCAGCTTAACCTTTTACCGCGCAAGTCTGG 780  
 Db 721 gttaaagatcgcttttaaagatcggaattcagcttaaccttttaccgctgaagctgg 780  
 QY 781 AGAAGAGAACATATCAGCTGATTCAGGGAACACCTTATCCATGCGACAGACCC 840  
 Db 781 aagaagagaaacatatacgtgatTCAGGGAACACCTTATCCATGCGACAGACCC 840  
 QY 841 AATACACAGACAGCGAGAGATATGCGGATACGAAGATATTTCTGACGCTGGAAT 900  
 Db 841 aatacacagacagcgagagatatacgggagatacgaagatattctgacgctggat 900

QY 901 AATTGCTGAGAAAAAGATCTTAGCGCGGACACCCCTGCTCCAGTATACCTCCGCAA 960  
 Db 901 aattgctgagaaaaagatcttagcgcggacacccctgctccagatattcctccgcaa 960  
 QY 961 GAAATTCGCCGTGTACCAAGAAAGCGGAAGGGCGCACCCCGACGAGAAAGCAGGAA 1020  
 Db 961 gaaatttcgccgtgtaccagaaagcggaagggcgaccccgacgagaaagcagcgaa 1020  
 QY 1021 AAGAAGCGCCCTCCAGAAAGCTCGAGAGACATGACGACGACGCTTGTGAGAAAT 1080  
 Db 1021 aagaagcgccctccagaaagctcgagagacatgacgacgacgcttgtgagaat 1080  
 QY 1081 CTTGCGCCCTCCCGAAGACGAGAAAGTCCCGAGACACCGAGACGATGTATCCAAAC 1140  
 Db 1081 cttgcgcccctcccgaaagcgaaggtcccgagaaacacgagacgattgtccaaac 1140  
 QY 1141 TCGGATCTGACTATTTCAATGACATGCCCCCGGTATCCCGGTGAGAGACTATAA 1200  
 Db 1141 tcggatctgactatTTTCAATGACATGCCCCCGGTATCCCGGTGAGAGACTATAA 1200  
 QY 1201 AGTTCTAATGCGCTCTCCATGCGCATATTCGCGGCTGTGAGCCCTGCGGCTC 1260  
 Db 1201 agttctaatgctgctctccatgcgcatatttcgcggtgtgagccctgcggtctc 1260  
 QY 1261 GTGGGCGCTACTGTTTGGAGCATGTAATAATGGCGCGGTAGCTAA 1305  
 Db 1261 gtgggcgctactgTTTGGAGCATGTAATAATGGCGCGGTAGCTAA 1305

RESULT 4  
 AAC67867  
 ID AAC67867 standard; DNA; 1305 BP.  
 XX  
 AC AAC67867;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Recombinant fowlpox virus-related polynucleotide, SEQ ID NO: 19.  
 XX  
 KW Fowlpox virus; FPV; antiviral; antibacterial; vaccine;  
 KM Newcastle's disease; Marek's disease; infectious laryngotracheitis; ds.  
 OS Unidentified.  
 XX  
 PN US6136318-A.  
 PD 24-OCT-2000.  
 XX  
 PF 07-JUN-1995; 95US-0486414.  
 XX  
 PR 26-FEB-1993; 93US-0024156.  
 PR 28-FEB-1994; 94WO-US02252.  
 XX  
 PA (JUNKER) JUNKER D E.  
 FA (COCH) COCHRAN M D.  
 XX  
 PI Cochran MD, Junker DE;  
 XX  
 DR WPI: 2000-686071/67.  
 XX  
 PT New recombinant fowlpox virus useful as vaccines contains foreign DNA  
 XX inserted into specific non-essential region of the genome  
 PS Disclosure: Column 77-80; 56pp; English.  
 XX  
 CC The present sequence is provided in a specification relating to a  
 CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted  
 CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA  
 CC can be expressed in host cells infected with FPV. The recombinant FPV  
 CC may be used in vaccines to protect animals (especially chickens) against  
 CC fowlpox and, depending on the source of the foreign DNA, other diseases,  
 CC particularly Newcastle's disease, Marek's disease or infectious

CC	laryngotracheitis.
XX	
SQ	Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

Query Match	Similarity	100.0%	Score 1305;	DB 21;	Length 1305;
Best Local	Similarity	100.0%	Pred. No. 0;		
Matches 1305;	Conservative	0;	Mismatches	0;	Indels
					Gaps
					0
QY	1	ATGCACCGTCCATCTAGACGACGACCTGCTTACTACGCGAAGAGAGGTGCTTAAC	60		
Db	1	atgacacgttcctcatctctcaagcagcacttcgcttactaagcgaaagagtgcttaac	60		
QY	61	AAACACATGATGTGGGTGGAAAACGGTGTCTAGCGGACGCTGTATTCCTTTTC	120		
Db	61	aaacacatgattgctggtgaaacggtgctcgaagcgacgttattcaactcttc	120		
QY	121	TGGACTTGTGTCCAGATTATGCGGAGATATCTGTTGTACGCAACGCTATGACCGC	180		
Db	121	tggacttgtgtcagaattatcgaggaatatactcttgtaagcaacgtatgacgcg	180		
QY	181	CATTATTTTGGAGAAATGCTTTTGGACTATCTGACTGCTTTCTCTCTCTGCTAGCAG	240		
Db	181	cattatttttggagaatagcttcttggaactatcgtaactgtcttctctctgtacgcag	240		
QY	241	AGCACCGCCCGCTACGTAAGTATTTAGCCGCTGCGCGCTCGACGCGCTAAC	300		
Db	241	agcacccgcgcgtacacgtacactatttagcgcgtcgcgtcgcagcgcgtacaac	300		
QY	301	ATACCGGGGGTGGCGCGTATACGATACCTCACATAGGGTATCAAGAGCGTCGACGT	360		
Db	301	ataccggcggtctgagccgtatacaagatacccaactaagggtatacaaggctcgagcgt	360		
QY	361	GTGAGCTCAACCCGATTTCTAACGTGACGACATGATATCGCGCGCCAAAGAAAAGAG	420		
Db	361	gtcgagctcaaacccgatttctaagctgtagcagcatgatatcgcgccaaagaaaagag	420		
QY	421	AAGGGGGCCCTTTCGAGAGCCCTCGTCTGTGTGTTCTACGTATTTAAGGGCAGACGCGC	480		
Db	421	aagggggcccttctgaaagccctcgctcgtctgttcttcgtgtaaaaggcgacgacgyc	480		
QY	481	GAGGACAGTACTGTCCATCTATGAAAAGAGTACAGGAGTGTGGCAGCTACAACTG	540		
Db	481	gagagcaagtaactgtccaatctatgaaagaagtacaggaattggtcgagctaacactg	540		
QY	541	CTATCTGAATGCGCCGTTCAATCTGCACAGATGTGGCAGTGGACTATGTTCTTAGCACC	600		
Db	541	ctatctgaattgcgcgcttcaatctgcaagatgtggtgcagtgtactatgttcttagcacc	600		
QY	601	CTTGATATGCGGAATGCGGGGAGTATCTCTCCCAACGTGCGGCTCTCTGGC	660		
Db	601	cttgatattcgagaaagcgcggtgactgactaattctccccaactgtcgctctctgyc	660		
QY	661	CAATACTTGTGACCCCTGAAATCGGGAGATTGTGGCAAAAGCTCTGTAACTGTAGAA	720		
Db	661	caatacttgcgtgacccctgaaaaatcgggagatttgcgcaaacgctctgttaacttagaa	720		
QY	721	GTTAAACGATCGCTGTTTAAAGATCGGGTTCGACGCTTAACCTTTTACCGTCCAAATGCTGG	780		
Db	721	gttaacgactgcgtttaaagatcgggttcgcgcgactttaaacttlttaccgttcgaaatgctgg	780		
QY	781	ACAACAGAAAGTATCAACTGAGATTATCAAGCGCAACCTTTATTCGATCGACAGACAC	840		
Db	781	acaacagaaacgtatcagactggtattcaaggcgaaacacttlatccgatcgagacacc	840		
QY	841	AATACACAGACACGGGAGCAGCATATATCGGGGATACGAAGATATTTCTGCAGCGCTGAAT	900		
Db	841	aatacacgacacgcgagcagcatatctcgggatatacgaagatatcttcgcaagcgtcgaa	900		
QY	901	AATTGCTGAGAGAAAAGAAATCTTAGCGCCGCCAGACCTCTGTCACGATATAGCTCCCGCAA	960		
Db	901	aatttgcgtgaggaagaaatactcttggtcgcgccgaagacctctgcagatatagctccgcgaa	960		

QY	961	GAATTC	CCCGTGTGA	ACCAGAAA	GCGGAAGG	CGCACCCCGG	ACGCGAGAA	MAAGACG	CA	1020
Db	961	gaattc	cccgctgtga	accagaaa	gcggaagg	cgcaccccgga	cgcagaaag	cagcgaa		1020
QY	1021	AAGAAAG	CGCCCTCC	AGAAAG	CTCGGAG	GAGACATC	CAGGCG	AGAGGCTT	CTGACAA	1080
Db	1021	aagaag	cgccctcc	cagaaag	ctcggag	gagacatc	caggcg	agagcttc	tggagaa	1080
QY	1081	CCCTCCG	CGCCCTCC	CGAAGAC	GCAGAA	GTCCCGAG	ACACGAG	ACAGCAT	ATATCCA	1140
Db	1081	cctcgccg	ccctcccg	aagacg	agaa	gtcccg	agacac	cagacag	atgatcc	1140
QY	1141	TCGGATC	CTGACTTA	TATCAAT	GACATG	ACCGCCG	CGGTGAT	CCGCGTG	GAGAGACT	1200
Db	1141	tcgatact	cgtactata	tacaatga	tgcgcgcg	tgatccg	gtgagag	agactata		1200
QY	1201	AGTTCTA	TATGCGCT	TCTCCAT	GCCCAT	TTTGGCGG	CTTGTGA	CTGCGCG	GTC	1260
Db	1201	agttcta	tgctgcgt	tctccatg	cccatct	ctgcggt	ctgtgac	tgcgcg	tcgctc	1260
QY	1261	GTTGGG	GGCTAC	GTGTTG	GAGACAT	CGTAAAT	TGCGCG	CGTAG	CTAA	1305
Db	1261	gttggg	gctacg	tcttg	gagacat	cgtaaa	tgcgcg	ctagctaa		1305

```

XX RESULT 5
XX AA249300
XX ID AA249300 standard; cDNA; 1305 BP.
XX AC
XX AA249300;
XX DT 14-MAR-2000 (first entry)
XX DE
XX ILTV glycoprotein D (gd) gene.
XX
XX Fowlpox virus; FPV; recombinant; antigenic protein; expression;
XX Infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
XX Marek's disease virus; cytokine; promoter; homologous recombination;
XX homology vector; multivalent; live vaccine; glycoprotein D; ds.
XX
XX Infectious laryngotracheitis virus.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 1..1305
XX FT /tag=a
XX FT /product="Glycoprotein D (gd)"
XX
XX US6001369-A.
XX PN
XX 14-DEC-1999.
XX PD
XX 07-JUN-1995; 95US-0477459.
XX PF
XX
XX 26-FEB-1993; 93US-0024156.
XX PR
XX 28-FEB-1994; 94WO-US02252.
XX PR
XX
XX (SYTR ) SYNTRO CORP.
XX PA
XX
XX Junker DE, Cochran MD;
XX PI
XX WPI; 2000-071638/06.
XX DR
XX P-PSDB; AAY58184.
XX
XX Recombinant fowlpox virus useful as a vaccine for immunizing fowl
XX against Marek's disease, Newcastle disease, Infectious
XX Laryngotracheitis Virus and/or fowlpox
XX
XX Claim 5; Columns 77-80; 56pp; English.
XX
XX The invention relates to a recombinant fowlpox virus (FPV)
XX comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment
XX of the fowlpox virus genome. The foreign DNA is capable of being
XX expressed in a host cell into which the fowlpox virus has been
XX

```



```
FT CDS 4113..4445
FT /*tag= f
FT /label= ORF4
FT complement (4139..4519)
FT CDS /*tag= g
FT /label= ORF4_reverse_complement
FT misc_difference 4535
FT /*tag= h
FT /note= "base 4535 is given as 's' in the
FT specification"
FT CDS 4609..5487
FT /*tag= i
FT /label= g6_gene
FT 5697..8654
FT CDS /*tag= j
FT /label= g60_gene
FT complement (6948..7826)
FT CDS /*tag= k
FT /label= ORF6_reverse_complement
FT 8462..9766
FT /*tag= l
FT /label= gD_gene
FT 9874..10962
FT CDS /*tag= m
FT /label= gI_gene
FT complement (11017..11150)
FT CDS /*tag= n
FT /label= ORF8_reverse_complement
FT 11159..12658
FT CDS /*tag= o
FT /label= gE_gene
FT 12665..13447
FT CDS /*tag= p
FT /label= ORF10
FT misc_difference 13002..13003
FT /*tag= q
FT /note= "bases 13002-13303 are given as 'ss' in
FT the specification"
FT repeat_region 13372..13473
FT /*tag= r
FT /function= terminal repeat region
FT
FT W09508622-A1.
FT
FT 30-MAR-1995.
FT
FT 16-SEP-1994; 94WO-US10628.
FT
FT 24-SEP-1993; 93US-0126597.
FT
FT (SYTR ) SYNTRO CORP.
FT
FT Cochran MD, wild MA:
FT
FT WPI: 1995-139591/18.
FT P-PSDB: AAM00630, AAM00631, AAM00632, AAM00633, AAM00634, AAM00635,
DR AAM00636, AAM00637, AAM00638, AAM00639, AAM00640, AAM00641 W00642.
XX
XX Recombinant attenuated infectious laryngotracheitis virus - for use
XX in vaccines to protect poultry from infection from the virus, also
XX methods of distinguishing between vaccinated and naturally infected
XX birds
XX
XX Example 1: Page 79-94; 177pp; English.
XX
XX The unique short region (AAT33504) of infectious laryngotracheitis
XX virus (ILTUV) genomic DNA contains genes (see also AAT33505 and
XX AAT33510-13) that are associated with ILTV virulence. A deletion in
XX those genes, esp. the glycoprotein g6 gene, glycoprotein gI gene,
XX thymidine kinase gene, uS2 gene, uI47-like gene or the glycoprotein
XX g60 gene, will attenuate the ILTV. A gene for a foreign antigen may
XX be inserted into the uS2, uI47-like, ORF4, g6, g60 or gI gene to
XX produce a recombinant ILTV. Recombinant ILTV may be used as a
```

```
CC multivalent vaccine, esp. for use in poultry.
XX
SQ Sequence 13473 BP; 3390 A; 3582 C; 3547 G; 2951 T; 3 other;
Query Match 100.0%; Score 1305; DB 16; Length 13473;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGACCGCTCTCATCTCAGACGCGACTGCGTTACTACGGAAGAGAGGTGCTTAAAC
DB 8462 atgacccgcgccatctcagcagcgactcgcgttactaagcgaagagaggtcgttaac 8521
QY 61 AAACACATGATGATTCGGCGTGAAGAACGGTCTGCTACGGCGCAGCTGATCTCTTTTC 120
DB 8522 aaacacatgattcgcgttggaacggttcgtcagcgagcagcttaccctcttc 8581
QY 121 TGGACTTGTGAGGATTTGCGGGAGCATATCTGTTGTACGGACGCTATGGACGCGC 180
DB 8582 tggacttgtgagatTTGCGGGAGCATATCTGTTGTACGGACGCTATGGACGCGC 8641
QY 181 CATTTATTTTGAAGAAATGCTTTTGGACTATACGACTGCTTCTTCTGCTAGCCAG 240
DB 8642 catttattttgagaaatgcttttggactatcgtactcgtcttcttccctcgtagcag 8701
QY 241 AACACCGCGCGCGCTCACGTCAGACTACATTTTAAAGCCGTCGCGCGCTGACCGCTAAC 300
DB 8702 aacacccgCGCGCGCTCACGTCAGACTACATTTTAAAGCCGTCGCGCGCTGACCG 8761
QY 301 ATACCGCGGCTTGGCCCGCATTAACAGATACCTCACTAGAGGATTAAGAGCGTGCACGTT 360
DB 8762 ataccgCGGCTTGGCCCGCATTAACAGATACCTCACTAGAGGATTAAGAGCGTGCAC 8821
QY 361 GTGAGCTTCACACCGCATTTCTAACGTGACGACATGATATCGGCGCCAAAGAAAAGAG 420
DB 8822 gtgagctTCACACCGCATTTCTAACGTGACGACATGATATCGGCGCCAAAGAAAAG 8881
QY 421 AAGGGGGCGCCCTTTGAGAGCGCTCCGTCGTCGTTGCTACGATTAAGGCGACACAGCG 480
DB 8882 aaggggCGCCCTTTGAGAGCGCTCCGTCGTCGTTGCTACGATTAAGGCGACACAG 8941
QY 481 GAGGACAACTACTGTCATCTATAGAAAAGTACAGAGATGCGGACCTACACATG 540
DB 8942 gaggacAACTACTGTCATCTATAGAAAAGTACAGAGATGCGGACCTACACATG 9001
QY 541 CTATCTGAATGCGCGCTTCAATCTGCACAGATGTGGGACGTGATGTTCTAGACAC 600
DB 9002 ctatctGAATGCGCGCTTCAATCTGCACAGATGTGGGACGTGATGTTCTAGACAC 9061
QY 601 CTTGTATCGCAAAATGCGCGGAGACTGACTATATTTCTCCCACTGCTGCTGTGGC 660
DB 9062 cttgtatCGCAAAATGCGCGGAGACTGACTATATTTCTCCCACTGCTGCTGTGGC 9121
QY 661 CAATACTTGTGACCCCTGAAATCGGAGATTGCGCAAAACGCTCTGTAACTGTAGAA 720
DB 9122 caatactTGTGACCCCTGAAATCGGAGATTGCGCAAAACGCTCTGTAACTGTAGAA 9181
QY 721 GTTAAAGATCGCTGTTTAAAGATCGGCTGCAGCTTAACTTTTACCGTGAATGCTGG 780
DB 9182 gttaaagATCGCTGTTTAAAGATCGGCTGCAGCTTAACTTTTACCGTGAATGCTGG 9241
QY 781 ACAACAGAACGATATACAGACTGATTTCAAGGCGAAACACTTTATCCGATGCAACAC 840
DB 9242 acaacagAACGATATACAGACTGATTTCAAGGCGAAACACTTTATCCGATGCAACAC 9301
QY 841 AATACACGACAGCGGACGACGATATATCGGGATATGGAAGATATCTCAGCGCTGAGAT 900
DB 9302 aatacagACAGCGGACGACGATATATCGGGATATGGAAGATATCTCAGCGCTGAGAT 9361
QY 901 AATTTGCTGAGGAAAAGATCTTAGCGCGCAGACCTCTGCTCAGATAGGCTCCCGCAA 960
DB 9362 aatttgCTGAGGAAAAGATCTTAGCGCGCAGACCTCTGCTCAGATAGGCTCCCGCAA 9421
```

QY 961 GAAATTCCTCGTGTACCCAGAAAGCGAAGGCCACCCCGAGCAGAAAGCAGCGAA 1020  
 Db 9422 gaattcccgctgaaccaagaagcggaagcgacccccgcgacgagaagcagcgaa 9481  
 QY 1021 AAGAAGGCCCCCTCCAGAAAGCTCGAGAGCAGACATGACGACAGAGCTTCTGAGAAAAT 1080  
 Db 9482 aagaagccccctccagaagactcggaaagacatgcagcagcagagcgtctctggaagaat 9541  
 QY 1081 CTTGCCGCCCTCCCGAAGAGCAGAGTCCCGAGAGACGAGACAGATGATCCCAAC 1140  
 Db 9542 cctgcgcgcctcccggaagcagcgaagtcctccggaagacacgagacgagatgccaaac 9601  
 QY 1141 TCGGATCTGACTATTCATGACATGCCCCGCGTATCCCGGTGAGAGAGACTACTAA 1200  
 Db 9602 tcggatctcgactatctacatgacatgcgcgcgtgatcccggtggaagagactactaa 9661  
 QY 1201 AGTTCTAATGCCGTCATGCCATATTCGCGGCTGTGTGATGCCGCGCTGCGCCTC 1260  
 Db 9662 agttctaattgcgctcccatgcatatccgcgcgtctgtagcctgcgcgctgcgcctc 9721  
 QY 1261 GTGGGCTACTGTTTGGAGCATGTAATGCGCGCTAGACTAA 1305  
 Db 9722 gtgggctactggttggagcatcgttaaatgctgcgcgctagctaa 9766

## RESULT 7

AAT4384  
 ID AAT44384 standard; DNA; 13473 BP.

AC AAT44384;

DT 02-JUN-1997 (first entry)

DE Infectious laryngotracheitis virus unique short region.

KM ILTV; vaccine; vector; attenuation; poultry;  
 KM avian infectious bronchitis virus; Newcastle disease virus;  
 KM Infectious bursal disease virus of chickens;  
 KM Marek's disease virus; herpesvirus; ss.

OS Infectious laryngotracheitis virus USDA strain 8302.

FT Key Location/Qualifiers

FT repeat\_region 1..273

FT misc\_RNA 274..13371

FT polyA\_signal 161..166

FT CDS

FT TATA\_signal

FT TATA\_signal

FT TATA\_signal

FT TATA\_signal

FT CDS

FT polyA\_signal

FT polyA\_signal

FT polyA\_signal

FT polyA\_signal

FT polyA\_signal

FT /note= "polyA signal for ORF2"  
 FT 2575..4107  
 FT /tag= k  
 FT /label= ORF3  
 FT /note= "unique long 47 (UL47)-like gene"  
 FT 4523..4526  
 FT /tag= l  
 FT /note= "TATA signal for ORF4"  
 FT 4113..4445  
 FT /tag= m  
 FT /label= ORF4  
 FT complement (4139..4519)  
 FT /tag= n  
 FT /label= ORF4(RC)  
 FT 4523..4526  
 FT /tag= o  
 FT /note= "TATA signal for ORF5"  
 FT 4609..5487  
 FT /tag= p  
 FT /label= ORF5  
 FT /note= "glycoprotein g6 gene"  
 FT 4609..4686  
 FT /tag= q  
 FT 4687..5484  
 FT /tag= r  
 FT 5564..5569  
 FT /tag= s  
 FT /note= "polyA site for ORF5"  
 FT 5653..5658  
 FT /tag= t  
 FT /note= "polyA signal for ORF5"  
 FT 5697..8654  
 FT /tag= u  
 FT /label= ORF6  
 FT /note= "glycoprotein g60 gene"  
 FT 6987..7727  
 FT /tag= v  
 FT /note= "repeat region consists of approx. 23  
 FT complement (6548..7826)  
 FT /tag= w  
 FT /label= ORF6(RC)  
 FT 8455..8458  
 FT /tag= x  
 FT /note= "potential TATA signal for ORF7"  
 FT 8461..9766  
 FT /label= ORF7  
 FT /note= "glycoprotein gD gene, alternative start  
 FT codon at 8633..8635"  
 FT 9819..9822  
 FT /tag= z  
 FT /note= "TATA signal for ORF8"  
 FT 9874..10962  
 FT /tag= aa  
 FT /label= ORF8  
 FT /note= "glycoprotein gI gene"  
 FT 9874..9939  
 FT /tag= ab  
 FT 9940..10959  
 FT /tag= ac  
 FT complement (10617..11150)  
 FT /tag= ad  
 FT /label= ORF8(RC)  
 FT 11069..11072  
 FT /tag= ae  
 FT /note= "TATA signal for ORF9"  
 FT 11159..12658  
 FT /tag= af  
 FT /label= ORF9  
 FT /note= "glycoprotein gE gene"  
 FT 11159..11212  
 FT /tag= ag

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FT mat_peptide 11213..12655
FT /**tag= ah
FT TATA_signal 12483..12486
FT /**tag= a1
FT /note= "TATA signal for ORF10"
FT CDS 12655..13447
FT /**tag= a1
FT /label= ORF10
FT repeat_region 13372..13743
FT /**tag= ak
XX MO629396-A1.
XX 26-SEP-1996.
XX 21-MAR-1996; 96WO-US03916.
XX 06-JUN-1995; 95US-0468190.
XX 23-MAR-1995; 95US-0410121.
XX (SYTR ) SYNPRO CORP.
XX Cochran MD, Wild MA;
XX WPI: 1996-443172/44.
XX P-PSDB: AAM06782;
XX P-PSDB: AAM06783;
XX P-PSDB: AAM06784;
XX P-PSDB: AAM06785;
XX P-PSDB: AAM06786;
XX P-PSDB: AAM06787;
XX P-PSDB: AAM06788;
XX P-PSDB: AAM06789;
XX P-PSDB: AAM06790;
XX P-PSDB: AAM06791;
XX P-PSDB: AAM06792;
XX P-PSDB: AAM06793.
XX Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G, g1 or US2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX Example 11; Page 88-103; 216pp; English.
XX The nucleotide sequence of 13,473 bp of contiguous DNA (AAT44384)
CC from the unique short region of infectious laryngotracheitis virus
CC (ILTV) contains the entire 13,098 bp unique short region and
CC includes 13 open reading frames that encode proteins (AAM06782-94) of
CC over 100 amino acids, 8 of which show significant homology to other
CC virus genes. Novel recombinant, attenuated ILTV comprises the ILTV
CC genome contg. a deletion in the unique short region, esp. in the
CC glycoprotein g6, g1, US2, ORF4, UL47-like or g60 gene. The
CC attenuated virus is useful as a vaccine against ILTV. A foreign
CC gene encoding an antigen e.g. from another avian virus can be
CC inserted into the US2, UL47-like, ORF4, g6, g60 or g1 gene to
CC provide a multivalent vaccine for chickens and other poultry.
CC Deletion of the g6 or g1 gene provides as a negative marker to
CC distinguish vaccinated from infected animals.
XX Sequence 13473 BP; 3390 A; 3581 C; 3547 G; 2952 T; 3 other:
SQ
Query Match 100.0%; Score 1305; DB 17; Length 13473;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 121 TGGACTTGTCTCAGGATTATCGGGAGCATATCTGCTTTGACCGCAACGCTATGACCGC 180
D 8582 tggactgtgtcagattatcgggagcatactgctttgacgcacacgctatgagcgc 8641
QY 181 CATTTATTTTGGAGAAATGTTTGGACTATCGACTGCTTCTTCCCTTCGCTAGCCAG 240
D 8642 cattatttttggagaaatgcttttggactatcgtaactgcttcttccctcagccag 8701
QY 241 AGACACCGCGCGTTCACGCTACGACTATCTTTAGGCGCTCGCGCTCGACGCGCTAAC 300
D 8702 agcacgcgcgcgtcacgtaactatacttaagccgctcgcgctcgcagcgtcaacc 8761
QY 301 ATACCGGGGTTGGCCCTATACAGATCTCACTAGGCTATCAAGAGCTGGGAGCTT 360
D 8762 ataccggggttggccctatacagatctcactaggtatcaaggaggtcgcagctt 8821
QY 361 GTGAGCTCAACCGGATTTCTAACGTGAGCAGCATGATATCGCGCGCCAAAGAAAAGAG 420
D 8822 gtgagctcaacccggatttctcaagctgagacatgatatcgcgccaaagaaaaagag 8881
QY 421 AAGGGGGCCCTTTCGAGCCCTCCGTCGTCTGTTCTACGTATTAAGGCGACGACGCGC 480
D 8882 aagggggccccttgcagccctccgctcgtctgattcagtgatlaaggcgacgacg 8941
QY 481 GAGGACAAAGTACTGTCCAAATCTATAGAAAAGATACAGGAAATGGCGAGCTCAACTG 540
D 8942 gaggacaaagtactgtccaaatctatagaaaagatagaggaaatgagcgagctcaactg 9001
QY 541 CTATCTGTAATCGCGCTCAATCTGACAGATGAGGAGTGAGCTATGTTCTCTAGCAC 600
D 9002 ctatctgtaatcgcgctcaatctgacagatgagggagtgagctatggttccctagcacc 9061
QY 601 CTTGTATTCGCAAAATGCGCGGAGCTGATATTTCTCCCACTGCTGCGCTCTTGCGC 660
D 9062 ctgtatctcgcaaaatgcgcgaggctgactatcttccccaactgctgcgtctctgcgc 9121
QY 661 CAATACCTTGTGACCCCTGAAAATGCGGAGATTTCGCGAAACAGCTTCGTACTCTAGAA 720
D 9122 caataccttgtgacccctgaaaatgcgggatttcgcaaaagactctgttaactctgaa 9181
QY 721 GTTACGATCGCTGTTTAAAGATCGGGTGCAGCTTAATCTTTTACCGTCAAGATGCTGG 780
D 9182 gttacgatcgctgttttaaagatcggttgcagcttaactttaccgtcgaaatgctgg 9241
QY 781 ACAACAGAAAGTATCAGACTGTGATTTCAAGGCAACCTTTATCCGATCGACAGACC 840
D 9242 acaacagaaagtatcagactgtgatttcaaggcaaccttaccgattcgagacacc 9301
QY 841 AATACAGACACGCGGAGCAGCTATATCGGGGATACGAAGATATTTGCAAGCTCGAAT 900
D 9302 aatcacagacacgcgagcagctatattcgggatacgaagatattcgcagcgcttgaat 9361
QY 901 AATTGTGAGAGAAAAGAAATCTTAGCGCGCCAGACCTCTGTCAGATAGGCTGCCGAA 960
D 9362 aattgtgagagaaaagaaatcttagcgcgccagacctctgttcagatagctccgcaa 9421
QY 961 GAAATTCOCGCTGTAAACCAAGAAACGGAAGGCGCACCCCGGACGCAAGAAAGCAGGAA 1020
D 9422 gaaatcccgctgttaaccaagaagacggaagggcgaccgccgagcaagaagcagga 9481
QY 1021 AAGAAGGCCCTCCAGAAAGACTCGGAGAGCAGCATGCAAGGCGCTTCTGGAAGAAAT 1080
D 9482 aagaagggccctccagaagactcggagagcacaatgaagggaggtcttcgagaaat 9541
QY 1081 CCTGCGCGCCCTCCCGGAAGAGAGAGTCCCGAGAGACACCGAGCAAGATGATCAAAAC 1140
D 9542 cctgcgcgcctcccggaagagacgaagttcccgagagacacgcagacagatccaaac 9601
QY 1141 TCGGATCTGACTATTAATGACATGACATGCCCCCTGTATCCCGGTGAGAGACTACTAA 1200
D 9602 tcggatctgactattaatgacatgacatgccccgtgatcccggtgagagactactaaa 9661
```

FT		/note="TATA signal for ORF4"
FT	CDS	6748..7080
FT		/*tag= o
FT		/label= ORF4
FT	CDS	complement (6774..7154)
FT		/*tag= p
FT		/label= ORF4(RC)
FT	TATA_signal	7158..7161
FT		/*tag= q
FT	CDS	/note="TATA signal for ORF5"
FT		7245..8123
FT		/*tag= r
FT		/label= ORF5
FT	sig_peptide	/note="glycoprotein g6 gene"
FT		7245..7322
FT		/*tag= s
FT	mat_peptide	7323..8120
FT		/*tag= t
FT	polyA_signal	8200..8205
FT		/*tag= u
FT		/note="polyA site for ORF5"
FT		8289..8294
FT	polyA_signal	/*tag= v
FT		/note="polyA signal for ORF5"
FT	CDS	8333..11290
FT		/*tag= w
FT		/label= ORF6
FT		/note="glycoprotein g60 gene"
FT		9623..10363
FT	repeat_region	/*tag= x
FT		/note="repeat region consists of approx. 23
FT		repeats of 30-36 bp"
FT	CDS	complement (9584..10462)
FT		/*tag= y
FT		/label= ORF6(RC)
FT	TATA_signal	11091..11094
FT		/*tag= z
FT		/note="potential TATA signal for ORF7"
FT	CDS	11098..12402
FT		/*tag= aa
FT		/label= ORF7
FT	TATA_signal	12455..12448
FT		/*tag= ab
FT	CDS	/note="TATA signal for ORF8"
FT		12510..13598
FT		/*tag= ac
FT		/label= ORF8
FT	sig_peptide	/note="glycoprotein g1 gene"
FT		12510..12575
FT		/*tag= ad
FT	mat_peptide	12576..13595
FT		/*tag= ae
FT	CDS	/note="complement (13253..13786)"
FT		/*tag= af
FT		/label= ORF8(RC)
FT	TATA_signal	13705..13708
FT		/*tag= ag
FT	CDS	/note="TATA signal for ORF9"
FT		13792..15291
FT		/*tag= ah
FT		/label= ORF9
FT	sig_peptide	/note="glycoprotein gE gene"
FT		13792..13845
FT		/*tag= ai
FT	mat_peptide	13846..15288
FT		/*tag= aj
FT	TATA_signal	15116..15119
FT		/*tag= ak
FT	CDS	/note="TATA signal for ORF10"
FT		15296..16080
FT		/*tag= al
FT	repeat_region	/label= ORF10
FT		16004..18912





Query Match	27.7%	Score 361	DB 13	Length 3502
Best Local Similarity	98.6%	Pred. No. 1.6e-104		
Matches 364	Conservative	0	Mismatches 5	Indels 0
			Gaps	0
QY	1	ATGCACCGTCCTCATCTCAGACGGCAGCTGCGTTACTACGCCAAGAGAGGTGCTTAAC	60	
DB	3134	atgcacgcgtccatctcagacgycactcgcttactacgcgaagagagtgcttaac	3193	
QY	61	AAACACATGATGGCGTGGGAAACGCGTCTGCTGACGGCGCGTATTCCTTTTC	120	
DB	3194	gaacacatgatgtggtggaagaaacggtgctcaagagcgcgtatlaactcttctc	3253	
QY	121	TGGACTTGTCGTAGATTATGCGGAGCATATCTGTTTGAAGCAGCATAGACCGC	180	
DB	3254	tgacttctgtatgaagattatgcggaagatctcttctgtacgaacgtatgacgcg	3313	
QY	181	CATTATATTTTGAAGATAGCTTTTGGACTATCGTACGCTCTTCTTCTGCTTACG	240	
DB	3314	catattttttgagaaatgcttcttgactatcgacagcttcttctctgcgtacgca	3373	
QY	241	AGCAGCGCGCGCGTACGATGATATTTTGGCGCTGCGCGCTGACGCGCTAAC	300	
DB	3374	agcaccgcgcgtacgactacattttagccgtcgcgctgcgacgcgtacac	3433	
QY	301	ATACGGGGGTTGGCGCTTAAAGATACGATCTCCTACGATGAGGATCAAGAGCTG	360	
DB	3434	ataccgcgcgttgcgcgtatacagaactcactaggtatcaagagctgcgagctt	3493	
QY	361	GTGAGCTC 369		
DB	3494	gtcgagctc 3502		
RESULT 10				
ID	AAT44399	standard; DNA: 42 BP.		
AC	AAT44399			
DT	03-JUN-1997	(first entry)		
DE	Homology vector 562-61.1F	junction B.		
ILTV	vaccine; homology vector 562-61.1F; attenuation; poultry;			
KM	avian infectious bronchitis virus; Newcastle disease virus;			
KW	infectious bursal disease virus of chickens;			
OS	Marek's disease virus; herpesvirus; glycoprotein gi; ss.			
XX	Chimeric infectious laryngotracheitis virus.			
Key	Location/Qualifiers			
FT	1..24			
FT	/tag= a			
FT	/label= ILTV			
FT	/note= "3", end of approx. 1619 bp Asp718T-XbaI			
FT	subfragment of the ILTV 8.0 kb Asp718I			

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FT      misc_RNA      19..42
FT      /*tag= b
FT      /label= ILTV
FT      /note= "5' end of approx. 691 bp XbaI-XhoI fragment
FT      of ILTV, generated by PCR"
XX      WO9629396-A1.
XX
XX      26-SEP-1996.
XX
XX      21-MAR-1996; 96WO-US03916.
XX
XX      06-JUN-1995; 95US-0468190.
XX      23-MAR-1995; 95US-0410121.
XX
XX      (SYTR ) SYNPRO CORP.
XX
XX      Cochran MD, Wild MA;
XX
XX      WPI; 1996-443172/44.
XX
XX      Recombinant infectious laryngotracheitis virus with deletion in the
XX      glycoprotein G, gI or US2 gene, etc. - useful for vaccines against
XX      infectious laryngotracheitis in poultry
XX
XX      Example 4; Fig 7B; 216pp; English.
XX
XX      Junction sequences (AAT44398-403) are provided of the DNA fragments
XX      used to construct homology vector 562-61.1F, a plasmid designed for
XX      the purpose of deleting a 983 bp portion of the glycoprotein gI
XX      gene from the unique short region (see also AAT44384) of infectious
XX      laryngotracheitis virus (ILTV), and replacing it with uida DNA.
XX      The vector incorporates a screenable marker, the E. coli uida gene,
XX      flanked by ILTV DNA. The homology vector is used to construct
XX      attenuated ILTV S-ILT-011, which is useful as a killed vaccine to
XX      protect chickens from ILTV disease and as a negative marker to
XX      distinguish vaccinated from infected animals. It is also used to
XX      construct S-ILT-013, which also has a deletion in the gC gene.
XX
XX      Sequence 42 BP; 12 A; 11 C; 8 G; 11 T; 0 other;
XX
XX      Query Match      3.2%; Score 42; DB 17; Length 42;
XX      Best Local Similarity 100.0%; Pred. No. 0.0019;
XX      Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      695 CGCAACAGCTCTGTAAGTCTAGAGTTAAGATCGCTGTT 736
XX      1 cgcacacagctctcgtactactagtagttaaagtcgctgtt 42
XX
XX      Db
XX
XX      RESULT 11
XX      ID      AAO21833 standard; DNA: 390 BP.
XX      AC      AAO21833;
XX
XX      DT      08-JUN-1992 (first entry)
XX
XX      DE      Randomising oligonucleotide used in SPERT mRNA prepn.
XX
XX      KM      Systematic polypeptide evolution by reverse translation; SPERT;
XX      ligand binding; ss.
XX
XX      OS      Synthetic.
XX
XX      PN      WO9202536-A.
XX
XX      PD      20-FEB-1992.
XX
XX      PF      01-AUG-1991; 91WO-US05463.
XX
XX      PR      02-AUG-1990; 90US-0561968.
XX

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XX      (COLS ) UNIV OF COLORADO.
XX
XX      Gold L, Tuerk C;
XX
XX      WPI; 1992-080018/10.
XX
XX      New method of systematic polypeptide evolution by reverse
XX      translation - by linking each polypeptide in sample mixt. to
XX      individualised mRNA allowing further synthesis of selected
XX      polypeptide(s)
XX
XX      Example; Page 55; 102pp; English.
XX
XX      The sequence is that of an example randomising oligonucleotide which
XX      is used in the prepn. of mRNA encoding candidate polypeptides for the
XX      method of systematic polypeptide evolution by reverse translation
XX      (SPERT). The method provides a rapid way of isolating and identifying
XX      polypeptide ligands which bind to target mols. The polypeptide ligands
XX      can be used in e.g. assay methods, diagnostic procedures, cell sorting,
XX      as activators or inhibitors of target mol. function, as probes, as
XX      sequestering agents, drug delivery vehicles, modifiers of hormone
XX      action and as catalysts. See also AAO21830-Q21832.
XX
XX      Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
XX
XX      Query Match      3.2%; Score 41.6; DB 13; Length 390;
XX      Best Local Similarity 51.6%; Pred. No. 0.0086;
XX      Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
XX
XX      QY      1003 GAGCAGAAACAGCGAAAGAGCCCTCCAGAAAGCTCGAGAGAGCATCGAGCA 1062
XX      1111 11 1 111 1 1 1 1 111 11 11111 1
XX      Db      201 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 260
XX      1063 GAGCCTTGTGAGAAATCTGCCGCCCTCCCGAAGCAGAGTCGCCGAGACACC 1122
XX      11 11 1 1 1 1 1 1 1 1 1 1 1111111 1 111 11 1
XX      Db      261 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 320
XX      QY      1123 GAGCAGCATGATCCAAACTCGATCTGACTATTACATGACATGCCCGGTGATCCG 1182
XX      11 1111 11 11 11 111 1 1111 11111 1 11
XX      Db      321 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 380
XX      QY      1183 GTGG 1186
XX      111
XX      Db      381 atgg 384
XX
XX      RESULT 12
XX      ID      AAO36859 standard; DNA: 390 BP.
XX      AC      AAO36859;
XX
XX      DT      22-JUN-1993 (first entry)
XX
XX      DE      PCR primer for 5' fixed sequence contg. T7 promoter and RBS.
XX
XX      KM      Systematic peptide evolution by reverse translation; SPERT; ligand;
XX      specific; inhibitors; probes; assay; cell sorting; ss.
XX
XX      OS      Synthetic.
XX
XX      PN      WO9303172-A.
XX
XX      PD      18-FEB-1993.
XX
XX      PF      31-JAN-1992; 92WO-US00801.
XX
XX      PR      01-AUG-1991; 91US-0739055.
XX
XX      PA      (UVRE-) UNIV RES CORP.
XX

```

PI Gold L, Prihnow D, Smith JD, Tuerk C;  
XX  
DR WPI: 1993-076529/09.  
XX  
PT Systematic polypeptide evolution by reverse translation - used  
PT for prodn. of polypeptide ligand specific for desired target  
PT molecule  
XX  
PS Example 1; Page 84; 98pp; English.  
XX  
CC SPERT is used to select novel polypeptides that bind the antibody  
CC of the epitope commonly recognised by the antisera from autoimmune  
CC mice which are the f1 progeny of a cross of NZB and NZW parents  
CC (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope  
CC consists of ca. 10 amino acids at the N-terminus of the histone H2B  
CC protein. To make mRNA encoding candidate polypeptides a 5' fixed  
CC sequence composed of a T7 promoter sequence and a ribosome binding  
CC site which is recognised by both prokaryotic and eukaryotic ribosomes,  
CC terminating in a restriction endonuclease site is synthesised and cloned  
CC using a number of oligonucleotides (example shown). A 3' fixed sequence  
CC is placed into a restriction site to provide an mRNA encoding the C-  
CC terminal trailer sequence of ca. 100 nucleotides lacking stop codons.  
CC In addition, a 3' primer annealing site is provided so that cDNA  
CC synthesis can be accomplished on the mRNA recovered from partitioned  
CC ribosome complexes. See also AAQ36845-63.  
XX  
SQ Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;  
  
Query Match 3.2%; Score 41.6; DB 14; Length 390;  
Best Local Similarity 51.6%; Pred. No. 0.0086;  
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
  
QY 1003 GACGCAAGAAAGCGAAAGAGCCCTCCAGAAAGACTCGAGAGACGATGCAGGCA 1062  
DB 201 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 260  
QY 1063 GAGGCTTTCGAGAAAATCTGCGCCCTCCGGAAGACGAGCAAGTCCCGAGACACC 1122  
DB 261 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 320  
QY 1123 GACACAGATGATCCAAACTCGACTGACTATTACATGATGATGCCCGCGTATCCCG 1182  
DB 321 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 380  
QY 1183 GTGG 1186  
DB 381 atgg 384  
  
RESULT 13  
AAAF6910  
ID AAF6910 standard; DNA; 390 BP.  
XX  
AC AAF6910;  
XX  
DT 29-MAY-2001 (first entry)  
XX  
DE Sequence containing a 120 repeat of ACG flanked by fixed fragments.  
XX  
DE ligand isolation; systemic polypeptide evolution by reverse translation;  
KM SPERT; ss.  
XX  
OS Synthetic.  
XX  
PN US6194550-B1.  
XX  
PD 27-FEB-2001.  
XX  
PF 23-NOV-1998; 98US-0197649.  
XX  
PR 31-JAN-1992; 92US-0829461.  
PR 02-AUG-1990; 90US-0561968.

PR 01-AUG-1991; 91US-0739055.  
XX  
PA (GOLD/) GOLD L.  
PA (TUER/) TUERK C.  
PA (PRIH/) PRIHNOW D.  
PA (SMIT/) SMITH J D.  
XX  
PI Gold L, Tuerk C, Prihnow D, Smith JD;  
XX  
DR WPI: 2001-243412/25.  
XX  
PT Isolating a polypeptide ligand to a target molecule, useful for  
PT diagnostic assays, comprises partitioning candidate mixtures comprised  
PT of ribosome complexes or mRNA-polypeptide copolymers relative to their  
PT affinity to the target molecule  
XX  
PS Example; Column 39; 35pp; English.  
XX  
CC The present sequence was used in an example illustrating an invention  
CC relating to a method for isolating a polypeptide ligand for a desired  
CC target molecule. The method involves synthesizing a nucleic acid mixture  
CC comprising mRNA having translatable and non-translatable regions and a  
CC mixture of nucleic acid polypeptide copolymers, each comprising the mRNA  
CC and a polypeptide encoded by its associated mRNA. The copolymers are  
CC partitioned relative to their affinity to the target. The method is  
CC termed systemic polypeptide evolution by reverse translation (SPERT).  
CC The polypeptides ligands of small molecule targets are useful in assay  
CC methods, diagnostic procedures, cell sorting, as inhibitors of target  
CC molecule function, as probes, as drug delivery vehicles and modifiers of  
CC hormone action and have therapeutic uses as sequestering agents. The  
CC target molecules include natural and synthetic polymers, including  
CC proteins, hormones, receptors and cell surfaces, nucleic acids and small  
CC molecules such as drugs, metabolites, cofactors and toxins. Polypeptide  
CC ligands are isolated and rapidly identified by this method.  
XX  
SQ Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;  
  
Query Match 3.2%; Score 41.6; DB 22; Length 390;  
Best Local Similarity 51.6%; Pred. No. 0.0086;  
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
  
QY 1003 GACGCAAGAAAGCGAAAGAGCCCTCCAGAAAGACTCGAGAGACGATGCAGGCA 1062  
DB 201 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 260  
QY 1063 GAGGCTTTCGAGAAAATCTGCGCCCTCCGGAAGACGAGCAAGTCCCGAGACACC 1122  
DB 261 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 320  
QY 1123 GACACAGATGATCCAAACTCGACTGACTATTACATGATGATGCCCGCGTATCCCG 1182  
DB 321 gacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 380  
QY 1183 GTGG 1186  
DB 381 atgg 384  
  
RESULT 14  
AAC44461  
ID AAC44461 standard; DNA; 1761 BP.  
XX  
AC AAC44461;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Zea mays DNA fragment SEQ ID NO: 42909.  
XX  
KM Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic;  
KM pathway; promoter; termination sequence; corn; ss.  
XX

```
OS      Zee mays subsp. mays.
XX      EPI033405-A2.
XX      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-0301439.
XX
PR      25-FEB-1999; 99US-0121825.
PR      05-MAR-1999; 99US-0123180.
PR      09-MAR-1999; 99US-0123548.
PR      23-MAR-1999; 99US-0125788.
PR      25-MAR-1999; 99US-0126264.
PR      29-MAR-1999; 99US-0126785.
PR      01-APR-1999; 99US-0127462.
PR      06-APR-1999; 99US-0128234.
PR      08-APR-1999; 99US-0128714.
PR      16-APR-1999; 99US-0129845.
PR      19-APR-1999; 99US-0130077.
PR      21-APR-1999; 99US-0130449.
PR      23-APR-1999; 99US-0130510.
PR      23-APR-1999; 99US-0130891.
PR      28-APR-1999; 99US-0131449.
PR      30-APR-1999; 99US-0132048.
PR      30-APR-1999; 99US-0132407.
PR      04-MAY-1999; 99US-0132484.
PR      05-MAY-1999; 99US-0132485.
PR      06-MAY-1999; 99US-0132486.
PR      06-MAY-1999; 99US-0132487.
PR      07-MAY-1999; 99US-0132863.
PR      11-MAY-1999; 99US-0134256.
PR      14-MAY-1999; 99US-0134218.
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PR      14-MAY-1999; 99US-0134370.
PR      18-MAY-1999; 99US-0134768.
PR      19-MAY-1999; 99US-0134941.
PR      20-MAY-1999; 99US-0135124.
PR      21-MAY-1999; 99US-0135353.
PR      24-MAY-1999; 99US-0135629.
PR      25-MAY-1999; 99US-0136021.
PR      27-MAY-1999; 99US-0136392.
PR      28-MAY-1999; 99US-0136782.
PR      01-JUN-1999; 99US-0137222.
PR      03-JUN-1999; 99US-0137528.
PR      04-JUN-1999; 99US-0137502.
PR      07-JUN-1999; 99US-0137724.
PR      08-JUN-1999; 99US-0138094.
PR      10-JUN-1999; 99US-0138540.
PR      10-JUN-1999; 99US-0138847.
PR      14-JUN-1999; 99US-0139119.
PR      16-JUN-1999; 99US-0139452.
PR      16-JUN-1999; 99US-0139453.
PR      17-JUN-1999; 99US-0139492.
PR      18-JUN-1999; 99US-0139454.
PR      18-JUN-1999; 99US-0139455.
PR      18-JUN-1999; 99US-0139456.
PR      18-JUN-1999; 99US-0139457.
PR      18-JUN-1999; 99US-0139458.
PR      18-JUN-1999; 99US-0139459.
PR      18-JUN-1999; 99US-0139460.
PR      18-JUN-1999; 99US-0139461.
PR      18-JUN-1999; 99US-0139462.
PR      18-JUN-1999; 99US-0139463.
PR      18-JUN-1999; 99US-0139750.
PR      18-JUN-1999; 99US-0139763.
PR      21-JUN-1999; 99US-0139817.
PR      22-JUN-1999; 99US-0139899.
PR      23-JUN-1999; 99US-0140353.
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PR      29-JUN-1999; 99US-0140991.
PR
PR      30-JUN-1999; 99US-0141287.
PR      01-JUL-1999; 99US-0141842.
PR      01-JUL-1999; 99US-0142154.
PR      02-JUL-1999; 99US-0142055.
PR      06-JUL-1999; 99US-0142390.
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PR      12-JUL-1999; 99US-0142977.
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PR      15-JUL-1999; 99US-0144005.
PR      16-JUL-1999; 99US-0144085.
PR      16-JUL-1999; 99US-0144086.
PR      16-JUL-1999; 99US-0144325.
PR      19-JUL-1999; 99US-0144331.
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PR      19-JUL-1999; 99US-0144335.
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PR      22-JUL-1999; 99US-0145192.
PR      23-JUL-1999; 99US-0145145.
PR      23-JUL-1999; 99US-0145218.
PR      23-JUL-1999; 99US-0145224.
PR      26-JUL-1999; 99US-0145276.
PR      27-JUL-1999; 99US-0145913.
PR      27-JUL-1999; 99US-0145918.
PR      27-JUL-1999; 99US-0145919.
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PR      03-AUG-1999; 99US-0147038.
PR      04-AUG-1999; 99US-0147204.
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PR      05-AUG-1999; 99US-0147192.
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PR      09-AUG-1999; 99US-0147935.
PR      10-AUG-1999; 99US-0148171.
PR      11-AUG-1999; 99US-0148319.
PR      12-AUG-1999; 99US-0148341.
PR      13-AUG-1999; 99US-0148565.
PR      13-AUG-1999; 99US-0148684.
PR      16-AUG-1999; 99US-0149358.
PR      17-AUG-1999; 99US-0149175.
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PR      20-AUG-1999; 99US-0149723.
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PR      23-AUG-1999; 99US-0149930.
PR      25-AUG-1999; 99US-0150566.
PR      26-AUG-1999; 99US-0150884.
PR      27-AUG-1999; 99US-0151065.
PR      27-AUG-1999; 99US-0151066.
PR      27-AUG-1999; 99US-0151080.
PR      30-AUG-1999; 99US-0151303.
PR      31-AUG-1999; 99US-0151438.
PR      01-SEP-1999; 99US-0151930.
PR      07-SEP-1999; 99US-0152363.
PR      10-SEP-1999; 99US-0153070.
PR      13-SEP-1999; 99US-0153758.
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PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155138.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0156569.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158233.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
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PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

[illegible]

XX 26-MAR-2002 (first entry)  
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 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29309.  
 XX  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PE 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EM;  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB67506.  
 PT  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1; SEQ ID NO 29309; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB157737-AB172072).  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 1232 BP; 358 A; 319 C; 336 G; 219 T; 0 other;

[illegible]

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Job time: 5143 sec

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ID	AB111609 standard; CDNA; 1232 BP
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AC	AB111609;



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 29, 2002, 00:11:43 : Search time 65.96 Seconds  
(Without alignments)  
4859.790 Million cell updates/sec

Title: US-09-994-064-10

Perfect score: 1305  
Sequence: 1 ATGCACCGCTCCTCATCTCAG.....TAAATGCGCGGTAGCTAA 1305

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1305	100.0	1305	2	US-08-484-575A-19
2	1305	100.0	1305	3	US-08-477-459-19
3	1305	100.0	1305	3	US-08-479-869-19
4	1305	100.0	1305	3	US-08-486-414-19
5	1305	100.0	1305	5	PCT-US94-01826A-19
6	1305	100.0	1305	5	PCT-US94-02252A-19
7	1305	100.0	1305	5	PCT-US96-03916-10
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11	42	3.2	42	5	PCT-US96-03916-10
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14	37.4	2.9	2277	1	US-08-676-974-2
15	37.4	2.9	2277	1	US-09-098-487-2
16	37	2.8	1288	1	US-08-440-856A-9
17	36.2	2.8	2943	1	US-08-042-747A-7
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20	35.4	2.7	32207	4	US-08-757-669A-20
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23	34.8	2.7	1187	1	US-08-440-856A-2
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33	33.4	2.6	1100	3	US-09-248-335-53	Sequence 53, Appl
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43	32.2	2.5	2745	1	US-08-363-255-13	Sequence 1, Appl
44	32.2	2.5	2745	1	US-08-363-255-13	Sequence 13, Appl
45	32	2.5	4257	2	US-08-690-473-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-484-575A-19  
Sequence 19, Application US/08484575A  
Patent No. 5923558  
GENERAL INFORMATION:  
APPLICANT: Mark D. Cochran and David E. Junker  
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,575A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)278-0450  
TELEFAX: (212)391-0525  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
US-08-484-575A-19

Query Match 100.0%; Score 1305; DB 2; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dp	121	TGACATTGTGACGATTTATGCGGAGACAAATGCTGTTGTACGCAAGCTTATGACCGC	180
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Qy	421	AAGGGGGGCGCTTTGAGGCGCTCCGCTGCTGTTCTGATGATTAAGGGGAGACAGCGC	480
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Dp	841	AATACAGACACGCGGAGACGATATATCGGGATACGAAGATTTCTGACGCGTGGAAT	900
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RESULT 2
US-08-477-459-19
; Sequence 19, Application US/08477459
; Patent No. 6001369
;
GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1305
US-08-477-459-19

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-08-479-869-19  
Sequence 19, Application US/08479869  
Patent No. 6123949  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D, Mark D  
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,869  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/024,156  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq, John P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1305 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1305  
US-08-479-869-19

Query Match 100.0%; Score 1305; DB 3; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 ATACCGGCGGTGGCCGCTATTAACAGATACCTACTAGGATATCAAGAGGTGCGAGCTT 360  
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QY 361 GTGAGCTCAACCCGATTTCTTACGTGACGACATGATATGGCGCCCAAGAAAAGAG 420  
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QY 421 AAGGGGGGCGCTTTCGAGGCGCTCCGCTGTGTTCTAGTCAAGTAAAGGGGAGGAGCGC 480  
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QY 661 CAATACCTGCTGACCCCTGAAAATGGGAGATTTGGCAAAAGCTCTGTAAGTCTTAA 720  
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Db 721 GTTAAAGATGCTGTTTAAAGATGGGTGCGAGCTTAACTTTTAAAGTGAATGCTGG 780  
QY 781 ACAACAGACAGTATGACGTGATTTCAAGGGCAACCTTTATCCGATCGACAGACC 840  
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QY 901 AATTTGCTGAGAAAAGATCTAGCGCGCCAGACCTGCTGATAGCGCTGCGCA 960  
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QY 961 GAAATTCGCGCTTAACCAAGAAAGCGGAAAGGCGCACCCCGGAGCCAGAAAAGCAG 1020  
Db 961 GAAATTCGCGCTTAACCAAGAAAGCGGAAAGGCGCACCCCGGAGCCAGAAAAGCAG 1020  
QY 1021 AAGAAGGCGCCCTCCAGAAAGCTGAGAGACATGACAGGAGGCTTCTGAGAAAAT 1080  
Db 1021 AAGAAGGCGCCCTCCAGAAAGCTGAGAGACATGACAGGAGGCTTCTGAGAAAAT 1080  
QY 1081 CCTGCGCGCCCTCCAGAAAGCTGAGAGACATGACAGGAGGCTTCTGAGAAAAT 1140  
Db 1081 CCTGCGCGCCCTCCAGAAAGCTGAGAGACATGACAGGAGGCTTCTGAGAAAAT 1140  
QY 1141 TGGGATCCGCTATTAACATGATGCGCGCGCTGATCCCGTGGAGAGACTACTAA 1200  
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QY 1201 AGTTCTAATGCGCTGCTCAATGCTGATTTGCGGGTTCGTAGCTGCGCGCTGCGCTC 1260  
Db 1201 AGTTCTAATGCGCTGCTCAATGCTGATTTGCGGGTTCGTAGCTGCGCGCTGCGCTC 1260  
QY 1261 GTGGGGCTACTGCTGTTGAGCATGCTAAATGCGCGCTAGCTAA 1305  
Db 1261 GTGGGGCTACTGCTGTTGAGCATGCTAAATGCGCGCTAGCTAA 1305

RESULT 4  
US-08-486-414-19  
; Sequence 19, Application US/08486414B  
; Patent No. 6136318  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Mark D.  
; APPLICANT: Junker, David E.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF  
; FILE REFERENCE: 42771D  
; CURRENT APPLICATION NUMBER: US/08/486,414B  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Fowlpox virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(432)  
US-08-486-414-19

Query Match 100.0%; Score 1305; DB 3; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCGCTCTCATCTCAGACGCGCTGCTTCTACGGGAAAGAGAGTGGCTTAC 60  
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Db 781 acaacagacagatcagatgatttcaagcgcaacctttatccgaltccagtcagacacc 840
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QY 1261 GTGGGCTACTGTTGGAGCATGTAAAAATGCGCGCGTACTAA 1305
Db 1261 gtgggctactgttggagcatgtaaaaatgcgcgcgctactaa 1305

RESULT 5
PCT-US94-01826A-19
; Sequence 19, Application PC/TUS9401826A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525

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; TELLEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1305
PCT-US94-01826A-19

Query Match 100.0%; Score 1305; DB 5; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACCGCTCTCATCTCAGACGCGACTCGCGTTACTACGCGAAAGAGAGTCTTAAC 60
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Db 781 ACAACAGAACAGTATCAGACTGATTTCAAGGCGAACCTTTATCCGATCGCAGACACC 840
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Db 1201 AGTTCTATGCGCGCTCATATGCGCGAGCGGCTTGTAGCGCGCGGCGCGCTC 1260
Qy 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGCGGCTAGCTAA 1305
Db 1261 GTGGGGCTACTGTTTGGAGCATGCTAAATGCGCGGCTAGCTAA 1305

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# RESULT 6 PCT-US94-02252A-19

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; Sequence 19, Application PC/TUS9402252A
; GENERAL INFORMATION:
; APPLICANT: Syntro Corporation, et al.
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02252A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1305
PCT-US94-02252A-19

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Query Match 100.0%; Score 1305; DB 5; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 781 ACAACAGACATATCAGACTGATTTCAAGGGAACACTTTATCGATCGGAGACACC 840
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 QY 1261 GTGGGCGCTACTGTTTGAGAGCATGTAATAATGCGCGGTAGCTAA 1305  
 Db 1261 GTGGGCGCTACTGTTTGAGAGCATGTAATAATGCGCGGTAGCTAA 1305

RESULT 7  
 PCT-US96-03916-10  
 Sequence 10, Application PC/TUS9603916  
 GENERAL INFORMATION:  
 APPLICANT: Wild, Martha A.  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
 TITLE OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/03916  
 FILING DATE: 23-MAR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/126,597  
 FILING DATE: 24-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39116-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1305 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHEtical: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS

LOCATION: 1..1305  
 PCT-US96-03916-10  
 Query Match 100.0%; Score 1305; DB 5; Length 1305;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 841 AATACAGACAGCGGAGAGAGTATATCGGGGATACGAAGATATTCGACCGCTGGAAT 900  
 QY 901 AATTGCTGAGGAAAAAAGATCTAGCGCGCAGACCCCTGCTCAGATAGGCTCCGCAA 960  
 Db 901 AATTGCTGAGGAAAAAAGATCTAGCGCGCAGACCCCTGCTCAGATAGGCTCCGCAA 960  
 QY 961 GAAATTCCTGCTGTAACCAAGAAAGCGAGAGCGCCACCCCGAGCAGAAAGACGCGAA 1020

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Db 961 GAAATTCGCGCTGTACCAAGAAAGCGAAGGCGGACACCGCGAGGCAAGAAAGCGCGAA 1020
OY 1021 AAGAAGGCGCCCTCCGAAGAACTCGGAGGCGAGCATGACGAGCGCTTCTGAGAAAAAT 1080
Db 1021 AAGAAGGCGCCCTCCGAAGAACTCGGAGGCGAGCATGACGAGCGCTTCTGAGAAAAAT 1080
OY 1081 CCGTGGCGCCCTCCCGAAGACGAGCAAGTCCCGGAGGAGCACCGACAGCATGATCCAAAC 1140
Db 1081 CCGTGGCGCCCTCCCGAAGACGAGCAAGTCCCGGAGGAGCACCGACAGCATGATCCAAAC 1140
OY 1141 TGGGATCCGACTATTATTAAGATGATGCGCCGCGTATCCCGGTGGAGAGACTACTAA 1200
Db 1141 TGGGATCCGACTATTATTAAGATGATGCGCCGCGTATCCCGGTGGAGAGACTACTAA 1200
OY 1201 AGTTCTAAATGCCCTCCATGCGCCGCTATTTGGGGGCGTCTGTAAGCTGCGCGCTGCTC 1260
Db 1201 AGTTCTAAATGCCCTCCATGCGCCGCTATTTGGGGGCGTCTGTAAGCTGCGCGCTGCTC 1260
OY 1261 GTGGGGCTACTGTGTGGAGCATCGTAAATGCGCGCTAGCTAA 1305
Db 1261 GTGGGGCTACTGTGTGGAGCATCGTAAATGCGCGCTAGCTAA 1305

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# RESULT 8 PCT-US96-03916-1

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; Sequence 1, Application PC/TUS9603916
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARVIGOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1059..2489
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2575..4107

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4113..4445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4609..5487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5697..8654
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9874..10962
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11159..12658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12665..13447
; PCT-US96-03916-1

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Query Match 100.0%; Score 1305; DB 5; Length 13473;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8522 AACAACATGATGCGGAGGAGAAACGCTGCTGCTGAGGCGAGGCTGTTACTCTTTC 8581
OY 121 TGGACTTGTGTCAGATTAATGCGGAGGATATCTGCTTTGACCAACGCTATGACCGC 180
Db 8582 TGGACTTGTGTCAGATTAATGCGGAGGATATCTGCTTTGACCAACGCTATGACCGC 8641
OY 181 CATTTATTTTGGAGAGATGCTTTTGGACTATGCTACTGCTTTCTTCTGCTAGCCAG 240
Db 8642 CATTTATTTTGGAGAGATGCTTTTGGACTATGCTACTGCTTTCTTCTGCTAGCCAG 8701
OY 241 AGCACCGCGCGCTGACAGTACGATTTTAAAGCGCGCGCTGACGCGCTAAC 300
Db 8702 AGCACCGCGCGCTGACAGTACGATTTTAAAGCGCGCGCTGACGCGCGCTAAC 8761
OY 301 ATACCGGCGGTTGGCCCGGTATAAGATACCTCACTAGGCTATCAGAGGCTGCGAGCTT 360
Db 8762 ATACCGGCGGTTGGCCCGGTATAAGATACCTCACTAGGCTATCAGAGGCTGCGAGCTT 8821
OY 361 GTCGAGCTCAACCCGATTTTAAAGTGAAGATGATGATGCGGCGCAAGAAAGAG 420
Db 8822 GTCGAGCTCAACCCGATTTTAAAGTGAAGATGATGATGCGGCGCAAGAAAGAG 8881
OY 421 AAGGGGGCCCTTTCGAGGCCCTCCGCTGCTGTCTACGTGATTAAGGCGAGCGGC 480
Db 8882 AAGGGGGCCCTTTCGAGGCCCTCCGCTGCTGTCTACGTGATTAAGGCGAGCGGC 8941
OY 481 GAGGACAAGTACTGTCCATCTAATAGAAAGATGAGGAAATGAGGAAATGAGGAAATG 540
Db 8942 GAGGACAAGTACTGTCCATCTAATAGAAAGATGAGGAAATGAGGAAATGAGGAAATG 9001
OY 541 CTATCTGAATGCGCGCTTCAATCTGACAGATGAGGAGTGGAGTATGCTCTGACACC 600
Db 9002 CTATCTGAATGCGCGCTTCAATCTGACAGATGAGGAGTGGAGTATGCTCTGACACC 9061
OY 601 CTGTATCCGGAAGATGCGGCGGAGTACTATATTTCCCCACATGCTGCTGCTGCG 660
Db 9062 CTGTATCCGGAAGATGCGGCGGAGTACTATATTTCCCCACATGCTGCTGCTGCG 9121
OY 661 CAATCTGCTGACCTGAAATCGGAGATTTGGCAACAGCTCTGTAAGCTTAAGAA 720
Db 9122 CAATCTGCTGACCTGAAATCGGAGATTTGGCAACAGCTCTGTAAGCTTAAGAA 9181

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QY	721	GTAAACGATCGCTGTTTAAAGATGGGTGCACGTTAACTTTTACCGTGCGAAATGCTGG	780
Db	9182	GTTAACGATCGCTGTTTAAAGATGGGTGCACGTTAACTTTTACCGTGCGAAATGCTGG	9244
QY	781	ACAACAGAAAGATATTCAGACTGGATTTTCAAGGGCAACACCTTTATCCGATTCGACAGACC	840
Db	9242	ACAACAGAAAGATATTCAGACTGGATTTTCAAGGGCAACACCTTTATTCGATTCGACAGACC	9302
QY	841	AATACAGACACGCGGACGACGATATTCGGGGATACGAAAGATATTTCTGCAGCGCTGGAAAT	900
Db	9302	AATACAGACACGCGGACGACGATATTCGGGGATACGAAAGATATTTCTGCAGCGCTGGAAAT	9362
QY	901	AATTTGCGAGAGAAAGATTCCTACGCGCGCCAGACCTCTGTCAGATAGCGCTCCGCAA	960
Db	9362	AATTTGCGAGAGAAAGATTCCTACGCGCGCCAGACCTCTGTCAGATAGCGCTCCGCAA	9422
QY	961	GAATTTCCCGCTGTATACCAAGAAAGCGGAAGGGCGCACCCCGGACGCAGAAAGACGCGAA	1020
Db	9422	GAATTTCCCGCTGTATACCAAGAAAGCGGAAGGGCGCACCCCGGACGCAGAAAGACGCGAA	9482
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QY	1201	AGTTCTAATGCGCGTCTCCATATGCCCATATTCGGGGCTTGATAGCCTGCGCGGTGCGCGCTC	1262
Db	9662	AGTTCTAATGCGCGTCTCCATATGCCCATATTCGGGGCTTGATAGCCTGCGCGGTGCGCGCTC	9722
QY	1261	GTGGGGGCTACGTGTTTGAGACATCGTAAATATGGCGCGTAAAGCTAA	1305
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RESULT 9  
 PCT-US96-03916-59  
 : Sequence 59, Application PC/TUS9603916  
 GENERAL INFORMATION:  
 APPLICANT: Wild, Martha A.  
 APPLICANT: Cochran, Mark D.  
 TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNOTRACHEITIS VIRUS  
 TITLE OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/03916  
 FILING DATE: 23-MAR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/126,597  
 FILING DATE: 24-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 39116-A

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TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 278-0400
  TELEFAX: (212) 391-0525
  INFORMATION FOR SEQ ID NO: 59:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 18912 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    HYPOTHEetical: N
    ANTI-SENSE: N
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 697..1533
    OTHER INFORMATION:
  FEATURE:
    NAME/KEY: CDS
    LOCATION: complement (1900..2784)
    OTHER INFORMATION:
  FEATURE:
    NAME/KEY: CDS
    LOCATION: complement (2916..3605)
    OTHER INFORMATION:
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 3694..5124
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  FEATURE:
    NAME/KEY: CDS
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    NAME/KEY: CDS
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  FEATURE:
    NAME/KEY: CDS
    LOCATION: complement (17380..18216)
    OTHER INFORMATION:
  CDT-US96-03916-59

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	Query Match	Score 1305;	DB 5;	Length 18912;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1305; Conservative	0;	Mismatches	0;	Gaps 0;
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 QY 241 AGCACCGCCGCGCTCAGCTACGACTATTTAGCGCGTGCAGCGCTCAGCGCGCTAAC 300  
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 Db 11398 ATACCGCGGCTTGGCCGCTATACAGATACCTCCTAGGGTATCAGAGGCTGCGACGTT 11457  
 QY 361 GTGAGCTCAACCCGATTTTCAAGTGAGAGATGATATCGGGCGCAAGAAAAGAG 420  
 Db 11458 GTGAGCTCAACCCGATTTTCAAGTGAGAGATGATATCGGGCGCAAGAAAAGAG 11517  
 QY 421 AAGGGGGGCGCTTTCAGAGCGCTCGCTGCTGCTTCTACGTGATTAAGGGCGAGAGCGC 480  
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 QY 481 GAGGACAGATGCTGCTCAATCTATAGAAAAGATACAGGGAATGTGGCGAGCTAACACTG 540  
 Db 11578 GAGGACAGATGCTGCTCAATCTATAGAAAAGATACAGGGAATGTGGCGAGCTAACACTG 11637  
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 QY 601 CTGTCTATCGGAAATGCGCGGAGCTGACTATATCTCTCCCACTGCTGCGCTCTGCG 660  
 Db 11698 CTGTCTATCGGAAATGCGCGGAGCTGACTATATCTCTCCCACTGCTGCGCTCTGCG 11757  
 QY 661 CAATACCTTGGTGCACCTGAAATCGGAGATTTGGCAAAACAGCTCTGTAACCTAGAA 720  
 Db 11758 CAATACCTTGGTGCACCTGAAATCGGAGATTTGGCAAAACAGCTCTGTAACCTAGAA 11817  
 QY 721 GTTAAAGATCGGCTTAAAGATCGGCTGACAGCTTAACTTTTACCTGCAAACTCTG 780  
 Db 11818 GTTAAAGATCGGCTTAAAGATCGGCTGACAGCTTAACTTTTACCTGCAAACTCTG 11877  
 QY 781 ACAACGAGACAGTATGAGCTGATTTCAAGCGCAACACCTTTATCGATCGACAGACC 840  
 Db 11878 ACAACGAGACAGTATGAGCTGATTTCAAGCGCAACACCTTTATCGATCGACAGACC 11937  
 QY 841 AATACAGACAGCGGAGACGATATTCGGGGATACGAATATCTGAGGCGTGGAAAT 900  
 Db 11938 AATACAGACAGCGGAGACGATATTCGGGGATACGAATATCTGAGGCGTGGAAAT 11997  
 QY 901 AATTTGCTGAGAAAAAAGATCTTACCGCGGCGAGACCTCTGTCAGATAGCTCTCCGCA 960  
 Db 11998 AATTTGCTGAGAAAAAAGATCTTACCGCGGCGAGACCTCTGTCAGATAGCTCTCCGCA 12057  
 QY 961 GAAATTTCCGCTGTAAACCAAGAAAGCGAAGGGCGACCCCGGAGCGAGAAAGACGCA 1020  
 Db 12058 GAAATTTCCGCTGTAAACCAAGAAAGCGAAGGGCGACCCCGGAGCGAGAAAGACGCA 12117  
 QY 1021 AAGAAGCCCTCCAGAGACTCGAGAGACATGACAGGCGAGGCGTTCGGAAGAAAT 1080  
 Db 12118 AAGAAGCCCTCCAGAGACTCGAGAGACATGACAGGCGAGGCGTTCGGAAGAAAT 12177  
 QY 1081 CCTGCCGCTCTCCCGAAGACAGCAAGTCCCGAGAGACACGAGACAGATGATCAAAAC 1140  
 Db 12178 CCTGCCGCTCTCCCGAAGACAGCAAGTCCCGAGAGACACGAGACAGATGATCAAAAC 12237

QY 1141 TCGATCTCTACTATTAAATGACATGACCCCGCTGATCCCGGTGAGAGAGACTACTAAA 1200  
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 QY 1261 GTGGGGCTACTGTTTGGAGCATGTAATAATGCGCGCTAGCTAA 1305  
 Db 12358 GTGGGGCTACTGTTTGGAGCATGTAATAATGCGCGCTAGCTAA 12402

RESULT 10  
 US-08-232-463-14/c  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEFFLINGER, F.  
 ; APPLICANT: FALKNER, F. G.  
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/232,463  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,313  
 ; FILING DATE:  
 ; APPLICATION NUMBER: EP 91 114 300.6  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMD  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7218 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; CLONE: pTZ9Pc-F15  
 ; US-08-232-463-14

Query Match 3 4\*: Score 44.4: DB 1: Length 7218:  
 Best Local Similarity 6.6%, Pred. No. 0.0012;  
 Matches 24; Conservative 186; Mismatches 152; Indels 0; Gaps 0;

QY 718 GAACTTAACGATCCGCTTTTAAAGATCGGCTGAGCTTAACTTTTAACTGGAATGCG 777  
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 QY 778 TGGACAAAGAACAGTATGAGACTGATTTCAAGGCGAACACCTTTATTCGATCGCAGAC 837







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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 2002, 21:59:57 ; Search time 1809.52 Seconds  
(without alignments)  
9733.811 Million cell updates/sec

Title: US-09-994-064-10  
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Sequence: 1 ATGCACCGCTCTCATCTCAG.....TAAATGCGCGCTAGCTAA 1305

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: em_esthum:*
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4: em_estlin:*
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13: gb_gss:*
14: em_gss_hum:*
15: em_gss_inu:*
16: em_gss_vrt:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.4	3.2	958	12	CNS03PCF
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3	40.8	3.1	321	10	BG874723
4	40.8	3.1	529	12	AO876396
5	40.6	3.1	317	9	AA942788
6	40.2	3.1	212	9	AJ012890
7	40.2	3.1	865	10	BG345158
8	40	3.1	688	10	BF521413
9	40	3.1	915	12	CNS0322R
10	40	3.1	1101	12	CNS00K2
11	39.6	3.0	558	10	BF825826
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14	39.6	3.0	713	9	AV897918
15	39.6	3.0	715	9	AV892667
16	39.6	3.0	716	9	AV896867
17	39.6	3.0	1046	12	AG073741

18	39.4	3.0	451	9	AA552908
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29	38.2	2.9	317	9	AW291911
30	38.2	2.9	450	10	BI366211
31	38.2	2.9	478	10	BI356327
32	38.2	2.9	485	9	AA202831
33	38.2	2.9	492	10	BE510710
34	38.2	2.9	508	10	BI229580
35	38.2	2.9	509	10	BE518669
36	38.2	2.9	565	10	BI368667
37	38.2	2.9	574	9	AI515323
38	38.2	2.9	589	9	AI514749
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40	38.2	2.9	620	10	BI370037
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42	38.2	2.9	655	10	BI214686
43	38.2	2.9	656	10	BI367087
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#### ALIGNMENTS

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AA942788 EST198287  
AJ012890 EHEST023R  
BG345158 HVSME9001  
BF521413 EST458889  
AL25504 Tetraodon  
AL077673 Drosophila  
BF825826 MR2-HN003  
AV896003 AV896003  
AV901789 AV901789  
AV897918 AV897918  
AV892667 AV892667  
AV896867 AV896867  
AG073741 Pan trogl

958 bp DNA linear GSS 17-MAY-2000  
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044H14 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL254472 GI:7975484  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 958)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bonneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 958)  
Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
3 (bases 1 to 958)  
REFERENCE  
JOURNAL  
AUTHORS  
TITLE  
COMMENT  
JOURNAL  
COMMENT  
FEATURES  
source  
/organism="Tetraodon nigroviridis"

QY	969	CGCTTAACCAAGAAAGCGGAAGGCGCGACCCCGACGACAAAGCAAGCCGAAAGAAAGGC	1028
Db	106	CGCTAAGCCATTGAAGCCATTGGGGGGTCCCAAGAAAGCGCCCGCCCAAGAAAGGAGGC	165
QY	1029	CCCTCCAGAGACTGCGAGCAGCATGCGAGCGAGCGCTTTGAGAGAAAAATCTGCGCC	1088
Db	166	TCCCAAGAAAGCCCGCCCGCGCCCAAGAAAGGTGAGAGAGAGCATGATGACGACGA	225
QY	1089	CCCTCCGAGAGAGAGCAAGTACCGCGAGGACACCGACACGATGATCTCAACATCTGCATC	1148
Db	226	CCCTTTGGGTGAGACATGATGACGAGGAGAAAGAGAGGCTGCTAAGGCTCTTGTCTGCTAA	285
QY	1149	TGACTATTACAAATGACATGCGCCCGCGTATCCCGTGGAGAGACTACTAAAGTTCTTA	1208
Db	286	GCGCGCTGAGGCGCGCCAGCGCCGCAAGAGAGAAAGAAAGAACCGCGTGGAGGCTCGCA	345
QY	1209	TGCGCT 1214	
Db	346	GGTGT 351	
RESULT	3		
LOCUS	BC874723	321 bp	mRNA linear
DEFINITION	RC1-BT0254-120200-016-c08 BT0254	Homo sapiens	CDNA, mRNA sequence.
ACCESSION	BC874723		
VERSION	BC874723.1	GI:14251654	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 321) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. P., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J. J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.J. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-RC1-BT0254-120200-016-c08&t3=2000-02-12&t4=1) Seq primer: puc 18 forward High quality sequence start: 32 High quality sequence stop: 87. Location/Qualifiers 1. .321 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BT0254" /dev_stage="Adult" /note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
FEATURES	Source		
BASE COUNT	104 a	124 c	89 g
ORIGIN			4 t





Dp	33	TGCGGGAAACAGCAGCCAGCTGAGCCAAAGAATAAGCATGTGGCCAGACC	GAGAAAGCAGACA	92
Oy	1013	GCAGCGAAAAGAAAG-GCCCCCTCCAGAGACTGGGAGACGACATGCAGAGCGTTC		1071
Dp	93	CCCCTGGAAGGCCGGCCCGGAGGAGGAGTAAGAGGGGGCTCAGAGGTGGCAGGATGCA		152
Oy	1072	GGAGAAAAATCTTGCCGCCCTCCCGAAGACGAGAAATCCCGAGSACACGACGAT		1131
Dp	153	GCACCCGGTGACAGATGCCACTGCACCCCGGAGACGAGAGCCCAAGSCCCCGGAGAA		212
Oy	1132	GATCCAAACTCGATCTGACTATTACATATGATGCC		1170
Dp	213	GGCCCAAGCCCAACCTGACTTTATCGAGAGCTTGCCC		251
RESULT	6			
AJ012890		AJ012890	212 bp	mRNA linear EST 27-MAR-2000
LOCUS		EHEST023R Entamoeba histolytica HM-1:IMSS		Entamoeba histolytica
DEFINITION		cDNA, mRNA sequence.		
ACCESSION		AJ012890		
VERSION		AJ012890.1	GI:7330436	
KEYWORDS		EST.		
SOURCE		Entamoeba histolytica.		
ORGANISM		Entamoeba histolytica		
REFERENCE		Eukaryota; Entamoebidae; Entamoeba.		
AUTHORS		1 (bases 1 to 212)		
TITLE		Willhoeft,U., Buss,H. and Tannich,E.		
		Analysis of cDNA expressed sequence tags from entamoeba		
		histolytica: identification of two highly abundant polyadenylated		
		transcripts with no overt open reading frames		
		Proctist 150 (1), 61-70 (1999)		
JOURNAL		20187114		
MEDLINE		Contact: Tannich E		
COMMENT		Bernhard Nocht Institute for Tropical Medicine		
		Bernhard Nocht Str. 74, 20359 Hamburg, Germany.		
FEATURES		Location/Qualifiers		
source		1..212		
		/organism="Entamoeba histolytica"		
		/strain="HM-1:IMSS; ATCC 30459"		
		/db_xref="taxon:5759"		
		/clone.lib="Entamoeba histolytica HM-1:IMSS"		
		/note="vector: lambda ZAP"		
BASE COUNT		88 a 30 c 55 g 39 t		
ORIGIN				
Query Match		3.1%; Score 40.2; DB 9; Length 212;		
Best Local Similarity		54.4%; Pred. No.1.7;		
Matches		81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;		
Oy	1003	GACGCGAAGACGCGAAGAGAGGCCCCCTCCAGAGACTGGAGAGACATGCAGCA		1062
Dp	59	GACTTAGAAAACAATACACACAGCAATTCGAGAGACGATGACGACGACATATGACTTA		118
Oy	1063	GAGGCTTGTGGAGAAATCTGCGCCCTCCCGGAGACGAGAGTCCCGAGAGACAC		1122
Dp	119	GAAGCAGGAAGAAATGATGATGATGATGATGACGACGAAGAATGATGACGATGATGAC		178
Oy	1123	GAGCAGCATGATCCAACTCGATCTCTTA		1151
Dp	179	GACGACGATGATGATGACGAAGATGATGA		207
RESULT	7			
LOCUS		BG345158	865 bp	mRNA linear EST 22-OCT-2001
DEFINITION		HVSMeg0018018f Hordeum vulgare pre-anthesis spike EST library		
		HVCNDA00008 (white to yellow anther) Hordeum vulgare cDNA clone		
		HVSMeg0018018f, mRNA sequence.		
ACCESSION		BG345158		
VERSION		BG345158.2	GI:16318857	
KEYWORDS		EST.		

**SOURCE** barley.  
**ORGANISM** Hordeum vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae  
 ; Triticeae; Hordeum.  
**REFERENCE** 1 (bases 1 to 865)  
**AUTHORS** Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu  
 'Y', Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton  
 'R.D., Close, S.D., Oates, R. and Maltin, D.  
 Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex pre-anthesis spike cDNA library  
 Unpublished (2001)  
**JOURNAL** On Feb 27, 2001 this sequence version replaced gi:13157487.  
**COMMENT** Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Total hg bases = 412  
 Seq primer: AATTACCTCCTCAATAAGG  
 High quality sequence stop: 856.  
**FEATURES**  
 location/qualifiers  
 1..865  
 /organism="Hordeum vulgare"  
 /cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone="HVSMEG0018018f"  
 /clone\_lib="Hordeum vulgare pre-anthesis spike EST library  
 HVCNDA0008 (white to yellow anther)"  
 /tissue\_type="pre-anthesis spike"  
 /lab\_host="SOLR"  
 /note="Vector: lambdaZAP; site:1: EcoRI; Site:2: XhoI;  
 Plants were grown in the greenhouse at the University of  
 California, Riverside (Fenton, SJ Close, TJ Close). Whole  
 spike with awns trimmed were collected at white, green and  
 yellow anther stages (Fenton). Total RNA was prepared from  
 each pool, equal quantities of all three RNA pools were  
 combined, poly(A) RNA was purified from the mixture, one  
 primary unamplified cDNA library was made, and 1 million  
 pfu were in vivo excised to give Bluescript SK(-) cDNA  
 phagemids. These steps were performed in the TJ Close lab  
 (Choi) at the University of California, Riverside.  
 Phagemids were plated and picked at the Clemson University  
 Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins  
 and Wing) Plasmid DNA preparations, DNA sequencing and  
 sequence analysis were performed at CUGI (Wing, Yu, Frisch  
 'Henry, Simmons, Oates, Rambo, Maltin). The sequence has  
 been trimmed to remove vector sequence and contains a  
 minimum of 100 bases of phred value 20 or above. For more  
 details on library preparation and sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders Also  
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"  
 BASE COUNT 196 a 217 c 271 g 181 t  
 ORIGIN  
 Query Match 3.1%; Score 40.2; DB 10; Length 865;  
 Best Local Similarity 53.5%; Pred. No.3.1;  
 Matches 84; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
 QY 1002 GGAGCGAGAAAGCGAGAAAGAGGCCCTCCGAGAACTCGAGAGCAGCATGACAGGC 1061  
 ||||| || ||| ||| ||| ||| ||| ||||| |||||  
 Db 65 GGAGCGAGCGAGCGAGCGCGCGCGAGCGAGAAAGTGAAGAGAGAGACCGACGACGACGAGCA 124  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Y 1062 AGAGGCTTCTTGAGAGAAATCTCGCGCCCTCCCGGAGAGCAGCAGAGTCCCGAGGACAC 1121  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 125 CGATGAGCAGCAGCATGATGATGATGACGACGACGACGACGACGACGACGACGACGACGACCA 184  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY	1122	CGAGCAGCATGATCCAAACTGCAGCTCGACATTATTC	1158
Dd	185	GGATACACGACGACGCCCGCTTACC GG GACTGTGC	221
RESULT	8		
LOCUS	Bf521413	688 bp	mRNA linear EST 08-DEC-2000
DEFINITION	EST1458889 DStL Medicago truncatula cDNA clone pDStL-43GZ, mRNA sequence.		
ACCESSION	Bf521413		
VERSION	Bf521413.1	GI:11610096	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
	Euraytoya, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
REFERENCE	1 (bases 1 to 688)		
AUTHORS	Pedorova,M., Pierston,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.		
TITLE	ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borling Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243 Fax: 651 649 5058 Email: debbysepucini.crl.umn.edu University of Minnesota name: M78858e TIGR sequence name: MTFDH37K More information is available at: http://chrsys.tamu.edu/medicago Seq primer: SKmod (CTA gaa cta ggg gat cc).		
FEATURES	Location/Qualifiers		
SOURCE	1..688		
	/organism="Medicago truncatula"		
	/cultivar="genotype A17"		
	/db_xref="taxon:3880"		
	/clone="pDSIL-43GZ"		
	/cdate_1ib="DStL"		
	/tissue_type="leaves infected with Colletotrichum trifolii"		
	/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"		
	/lab_host="E. coli strain XLOLR"		
	/note="Vector: pluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."		
BASE COUNT	219 a 139 c 191 g 139 t		
ORIGIN			
Query Match	3.1%; Score 40; DB 10; Length 688;		
Best Local Similarity	52.4%; Pred. NO. 3.2;		
Matches	88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;		
OY	1003	GACGCAGAACAACAGCAAGCCCCCTCCAGAACCTCGAGAGACATGCAGGCA	1062
Dd	408	GGCAAAGAAAGTGAGGAGAGGTTGCTGCTGCAAAAGATGCAGAGGTAATAATCCACATCA	467
OY	1063	GAGGCTTCTGGAGAAATCTCTGCGCCGCTCCCGAAGACGACGAATGCTCCCGAGACACC	1122

[illegible]

	RESULT	10
CNS00KR2	LOCUS	
DEFINITION	CNS00KR2	1101 bp DNA linear GSS 03-JUN-1999
ACCESSION	Drosophila melanogaster genome survey sequence T7 end of BAC: BACR1F22 of Rpci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
VERSION	AL077673	
KEYWORDS	AL077673.1 GI:4957249	
SOURCE	GSS	
ORGANISM	fruit fly, Drosophila melanogaster	
AUTHORS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1101)	
TITLE	Genoscope.	
JOURNAL	Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutogo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named Rpci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	
FEATURES	Location/Qualifiers	
SOURCE	1..1101	
	/organism="Drosophila melanogaster"	
	/db_xref="taxon:7227"	
	/clone_1lb="RPCI-98"	
	/clone="BACR1F22"	
	/note="end : T7"	
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ORIGIN		
Query Match	3.1%; Score 40; DB 12; Length 1101;	
Best Local Similarity	10.0%; Pred. No. 3.9;	
Matches	Conservative 154; Mismatches 144; Indels 0; Gaps 0;	
OY	832 GCAGACACCATATACACGACGCCGCACGATATTTCGGGATACGAAGATTTTGTCCAG	891
DB	::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	757 KKAAGNMAAKAAGKAMDAAMAAMAAKADMAKAMMMMMGMMMMVKKMGKGKGM	816
OY	892 CGCTCGAATTAATTCTCGTGGAATAAGAATCTTAGCGGCCGACGACTCTGTCCAGATAC	951
DB	: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	817 MGRKNGKTMMKNVNKKGMAKNNKBMBAMMMMMMKMMNDKNNMCKTCSMMKKMT	876
OY	952 GTCCSCCAAGAAATTCCTCGCTGTAAACAAGAACGCGAAGGGCGACCCCGCAGCACAA	1011
DB	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	877 MMHMMMAKKMHNMKMMKMKHKHYNHKMMCHNGTCSMGCKKKMAKTKCBMMMAAKMAKV	936
OY	1012 AGCAGCAAAAAGAGGCCCCCTCCAGAAAGCTCGGAGAGCATGACAGGACAGAGCTTCT	1071
DB	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	937 ASMAADKKMDGMAKMIMGNCMGCMGMAAGKKMMMGAGVAMGGTAGKMMTMGTMAIMA	996
OY	1072 GGAGAAATTCCTCGCCGCTCCCGCAAGACGAGAACTCCCGCAGACACGAGACAGAT	1131
DB	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	997 KMAAGMAKHAYNMGNHMKNKVVNAMKKMMMKCMNNMKMKHNVMNMKMMMDKHAMNK	1056
OY	1132 GATCCAACCTGGATCTCTGATATTACATG	1162
DB	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
DB	1057 MACSMNKHMMAGKKKKVMMMMKKKMMVVND	1087

RESULT	11	558 bp	mRNA	linear	EST 13-JAN-2001
LOCUS	BF825826/c				
DEFINITION	BF825826	MR2-HN0036-171100-002-e03	HN0036	Homo sapiens	CDNA, mRNA sequence.
ACCESSION	BF825826				
VERSION	BF825826.1	GI:12168527			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 558)				
AUTHORS	Diag Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nages,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bata,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	200202663				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&tl2=MR2-HN0036-171100-002-e03&tl3=2000-11-17&tl4=1) Seq primer: puc.18 forward High quality sequence stop: 254.				
FEATURES	Location/Qualifiers				
source	1..558 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HN0036" /dev_string="Aguil" /note="Organ: head_normal; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	96 a 180 c 124 g 158 t				
ORIGIN					
Query Match	3.0%;	Score 39.6;	DB 10;	Length 558;	
Best Local Similarity	45.9%;	Pred. NO.3.8;			
Matches 135;	Conservative 0;	Mismatches 159;	Indels 0;	Gaps 0;	
870	GGGATACGAGATATTCTGCACGCGCTGCAGATATTCTGCGAGAAAAGATCTTAGCCG	929			
111	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
Db	397 GGGCGACCGCAAGAGAGATTTGGCTCTGTTGAAGCCCTTAAACAATAATAGTCTCTCGAG	338			
930	GCCNACCCCTGCTCCAGATAGGCGTCCCGCAAGAAATTCCTGTATACCAAGAAAGCGGA	989			
111	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
Db	337 TCCAAACCATTTGCTCGGAAAGCTGACCAAAAGAGACTGTCCAGACAGCTGGTAAAGAGG	278			
990	AGGGCGCACCCCGGACGCGAGAAAGCAGCGCAAAAGAGCCCTCCAGAGAGACTCGAGAGA	1049			
111	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
Db	277 ACCCGCAGTCCGATAGTAAGTGTCTCTCGAGGCGCAAGAGCCCGCAGACCTCGGACGTGATGA	218			
1050	CGACATCGACGCGAGAGGCTTCTGAGAGAAATCTCTGCGCCCTCCCGGAAGACGAGAGCT	1109			
111	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				

Db	217	GSAAAGGAGGAGGAGGAAGACTGTGAAGAAATGGTATGTGTAACCAAGCGGGAGCCTCTGGGG	158
Oy	1110	CCCCGAGGACACCAGCAGCATGATTCCAAATCTCGATCTGTACTATTACAATGA	1163
Db	157	CTCCGAGGACGATGCTGATACGCTGATGATGACTATGATGAGGAGCTGCATCCACTCTGA	104
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RESULT 12			
LOCUS	AV896003/c		
DEFINITION	AV896003 Nori Satoh unpublished cDNA library, young adult Clona intestinalis cdna clone rciad43115 3', mRNA sequence.	567 bp	mRNA linear EST 09-NOV-2001
ACCESSION	AV896003		
VERSION	AV896003.1 GI:16885099		
KEYWORDS	EST.		
SOURCE	Clona intestinalis.		
ORGANISM	Clona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona. 1 (bases 1 to 567)		
REFERENCE	Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T. Expressed genes in Clona intestinalis unpublished (2000) Contact: Nori Satoh Department of zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp.		
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<hr/>			
FEATURES			
source	location/Qualifiers		
	1..567		
	/organism="Clona intestinalis"		
	/db_xref="taxon:7719"		
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	/clone_lib="Nori Satoh unpublished cdna library, young adult"		
	/tissue_type="whole animal"		
	/dev_stage="young adult"		
BASE COUNT	140 a 148 c 87 g 192 t		
ORIGIN			
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Query Match 3.0%; Score 39.6; DB 9; Length 567;			
Best Local Similarity 50.0%; Pred.No.3.8;			
Matches 99; Conservative 0; Mismatches 99; Indels 0; Gaps 0;			
Oy	967	CCCGCTGTATACCAAAACCGAAGGGGCCACCCGGAGCGCAAGAAAGCAGCGAAAANG	1026
Db	480	CCAATGTAGAAGATATCTCAGCAAGAGGAGACAAAGAGGCAAGGGGAGAGAGGAA	421
Oy	1027	GCCCCTCCAGAGACTCGGAGGACGACATGCGAGGAGGCTTCTGSAAMAAATCCTGCC	1086
Db	420	GAAAGAGAAAGACGAGATGATGATGATGACGACGATGACGAAGATGATGATGATGAT	361
Oy	1087	GCCCTCCCCGAAGACGAGAGAACTCCCCGAGAGCACCCGACGACGATGATCCAAACTGGAT	1146
Db	360	GACGAAGATTAATGACGAGATGATGATGATGATGATGATGATGATGATGATGATGAT	301
Oy	1147	CCTGACTTTTCAATGAC 1164	
Db	300	GACGACGACGAAGATGAC 283	
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RESULT 13			
LOCUS	AV901789/c		
DEFINITION	AV901789 Nori Satoh unpublished cdna library, young adult Clona intestinalis cdna clone rciad52h17 3', mRNA sequence.	637 bp	mRNA linear EST 09-NOV-2001
ACCESSION	AV901789		
VERSION	AV901789.1 GI:16890887		
KEYWORDS	EST.		
SOURCE	Clona intestinalis.		

ORGANISM	Cliona intestinalis	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.
REFERENCE	1 (bases 1 to 637)	
AUTHORS	Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.	
TITLE	Expressed genes in Clona intestinalis	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers	
FEATURES	Source	
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OY	1027 GCCCCTCCAGAGATCGAGAGGACGACATGCGAGGAGAGCTTCGTGAGAAATCCGTGCC 1086	
Db	515 GAGAGGAGAGAGCAGCAGATGATGATATGACGACGTGACGAGATGATGATGATGATGAT 456	
QY	1087 GCCCTCCCCGAGAGAGAGAGTCCCGAGAGACCGAGACGATGATCCTCGAT 1146	
Db	455 GACGAAAGATATGACGACGATGATGATGACGAAATGATGATGATGATGATGATGATGAT 396	
QY	1147 CCTGACTATTACATGAC 1164	
Db	395 GACGACGAGCAAGATGAC 378	
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DEFINITION	AV897918 Nori Satoh unpublished cDNA library, young adult Clona	
ACCESSION	AV897918	
VERSION	AV897918.1	
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REFERENCE	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;	
AUTHORS	Phlebobranchia; Clonidae; Clona.	
TITLE	1 (bases 1 to 713)	
JOURNAL	Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.	
COMMENT	Expressed genes in Clona intestinalis Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers	

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Ddb	523	GAGAGGAAAGACGACCATGTGATGACAGAGAT	GAAGAGATGATGATGACGAAGATGAT	464
OY	1087	GCCCCTCCCGAAGACGACGAAAGTCCCGGAG	AACCCGACACCATGATCCAAACTGGGAT	1146
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ACCESSION	AV892667
VERSION	AV892667.1
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ORGANISM	Ciona intestinalis

ORGANISM  
Clona intestinalis, Chordata: Urochordata, Ascidiacea; Enterogona;  
Eukaryota, Metazoa, Chordata: Cephalochordata, Cephalochordata;  
Phlebobranchia, Clonidae, Clona.  
REFERENCE  
1 (pages 1 to 715) Satoh, Y., Kohara, Y. and Shin-i, T.  
TITLE  
Expressed genes in Clona intestinalis  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Nori Satoh

Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel.: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers

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D <sub>b</sub>	GACGACGACGAAGATGAC	393

Search completed: September 29, 2002, 00:52:16  
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OM of: US-09-994-064-11 to: GenEmbl:\* out\_format : pfs

Date: Sep 29, 2002 11:05 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

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gb_v1:HSMDGLXCO	+	2226.00	3510.76	3.5e-187	16372	U31965 Gallid herpesvirus-1 g
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VERSION	AR093367.1	GI:10020117			
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SOURCE	Unknown.				
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REFERENCE 1 (bases 1 to 1305)

AUTHORS Cochran,M.D. and Junker,D.E.

TITLE Recombinant fowlpox viruses and uses thereof

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AUTHORS 1 (bases 1 to 1305)
Cochran, M.D. and Junker, D.E.
TITLE Recombinant fowlpox viruses and uses thereof
JOURNAL Patent: US 6136318-A 19 24-OCT-2000;
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CDS

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 ACCESSION L31965  
 VERSION L31965.1 GI:493595  
 KEYWORDS glycoprotein D.  
 SOURCE Gallid herpesvirus 1.  
 ORGANISM Gallid herpesvirus 1.  
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.  
 1 (bases 1 to 1627)  
 REFERENCE Johnson, M.A., Tyack, S.G., Pridoux, C.T., Kongsuwan, K. and Sheppard, M.  
 Sequence characteristics of a gene in infectious laryngotracheitis virus homologous to glycoprotein D of herpes simplex virus DNA Seq. 5 (3), 191-194 (1995)  
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LOCUS A22122 3502 bp DNA linear PAT 22-JUN-1992
DEFINITION ILTV gp60 gene.
ACCESSION A22122
VERSION A22122.1 GI:583833
KEYWORDS
SOURCE
ORGANISM Gallid herpesvirus 1.
Virus: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
1 (bases 1 to 3502)
REFERENCE
AUTHORS
TITLE INFECTIOUS LARYNGOTRACHEITIS VIRUS VACCINE
JOURNAL Patent: WO 9203554-A 51 05-MAR-1992;
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ORIGIN

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Percent Similarity: 99.187 Percent Identity: 96.748

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US-09-994-064-11 x A22122 ..

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ACCESSION 104278  
VERSION 104278.1 GI:591810  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 1594)  
AUTHORS Bertman, P. W. and Lasky, L. A.  
TITLE Vaccines based on membrane bound proteins and process for making them  
JOURNAL Patent: EP 0139417-A1 2 02-MAY-1985;  
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ORIGIN

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89 GCCATTTTACGAGAGGAGGAGGCTATACAAAGTCTGTTTAAAGACAG 138  
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35 laValPheThrLeuPheThrCysValArgIleMetArgLysHis 50  
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139 GGGTTAGGAGTTGTTGGCTCAT.....AGCTTCAGCGGACGACCA 182  
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51 .....IleCysPheValArgAs 56  
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183 ACTACCCGATCATGATATCTTAAGTCTCTTTGTGTGCTGCTTC 232  
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56 naIleMetAspArgHisLeuPheLeuArgAsnAlaPheThrPheIleVal 73  
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233 CGGTATG..... 239  
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73 euLeuSerSerPheAlaSerGlnSerThrAlaAlaValThrTyraPyr 89  
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240 .....GGGGGGGCTGCCGACAGTTGGGGCGGTATTTGTTGTCTC 284  
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90 IleLeuGlyArgArg..... 94  
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285 ATAGTGGGCTTCATGGGTCCGCGCAAAATATGCTTGGCGGATGCTC 334  
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95 .....AlaL 96  
:::|::|  
335 TCTCAAGATGGCCGACCCCATCGCTTTCGCGCAAGACCTTCCGCTCC 384  
|||||  
96 euAspAlaLeuThrIlePro.....Ala 103  
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385 TGGACAGCTGACCAACCTCCGGGGGTCGCGGCTGTACCAATCCAG 434  
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104 ValGlyProTyrAsnArgTyr.....Le 111  
:::|::|  
435 GCGGCGCTACCGAACCCGTTCCAGCCGCCACGCTCCGATACGCTTTA 484  
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111 uThrArgValSerArgGlyCysAspValValGluLeuAnProIleSer 128  
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485 CCGCGGTGTGAGAGCGCGCTGCCGACGCTGCTTAAACGACGCTCGG 534  
|||||  
128 snValAspAspMetIleSerAlaAlaLysGluLysGluLysGlyPro 144  
:::|::|  
535 AGGCCCCCGAGTTGTCCGGGGGCTCCGAGAGCTCGGAAACACACC 584  
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145 PheGluAlaSerValValThrPheTyrValIleLysGlyAspAspGlyG 161  
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585 TACACCTGACCATCGCTTGGTTCGAGT.....GAGG 619
161 uasplysTyrCysProIleTyrArgLysGluTyrArgLysGlyAspY 178
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620 CAACGTGTCTATCCCATCGGTATGAGTACACCGAATGCTCTACCA 659
178 alginLeuSerGlyCysAlaValAlaInserAlaInMetProAlaVal 194
    ::::: ||||| ||||| ||||| |||||
670 ACAAGTCTCTGGGGGCTGTCCATCCGACGACGAGCCGCTG..... 713
195 AspTyrValProSer...ThrLeuValSerArgAsnGlyAlaGlyLeuTh 210
    ::::: ||||| ||||| ||||| |||||
714 AACACTATGACAGCTTCAGCGCGTCAAGAGAGATACCTGGGGTCTT 763
210 rIlePheSerProThrAlaAlaLeuSerGlyInTyrLeuLeuThrLeu 227
    ::::: ||||| ||||| ||||| |||||
764 GATCAGACGCCCCCGCTTGAGACGCGCGGACCTACTCGGCTGCTGA 813
227 yslIleGlyArgPheAlaGlnThrAlaLeuValThrLeuGlu.....Val 241
    ||||| ::::: ||||| ||||| |||||
814 AGATAAACGACTGAGCGAGATATACAGTTTATCTGAGACCGAGCC 863
242 AsnAspArgCysLeuLysIleGlySerGlnLeuAsnPheLeuProSerLy 258
    ::::: ||||| ||||| ||||| |||||
864 AAGGCTCTCTGT...AAGTACACCTCCCGCTGCGCATCCCGCTCAGC 910
258 sCysTrpThrThrGlnGlnTyrGlnThrGly..... 268
    ||||| ::::: ||||| ||||| |||||
911 CTGCTCTCCCCCGAGCGCTACAGAGGCGGTGACGCTGAGACATCG 960
269 .....PheGlnGlyLeuHisLeuTyrProIleAlaAspThr 280
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961 GGATGCTGCCCCGCTTCATCCCGAGAACAGCGACCGCTCGCTATAC 1010
281 AsnThrArgHisAlaAspAspValTyrArgGlyTyrGluAspIleLeuG1 297
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1011 AGCTTGAAAGATCGCGGG..... 1028
297 nArgTrpAsnAsnLeuLeuArgLysLysAsnProSerAlaProAspPro 314
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1029 ....TGGCAC.....GGGCCCCAGGCCCCCA...TACA 1053
314 rGProAspSerValProGlnGlnIleProAlaValThrLysAlaGlu 330
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1054 CGAGCACCTGCTGCCCGCGAGCTGCC..... 1082
331 GlyArgThrProAspAlaGlnSerSerGlyLysLysAlaProGluAs 347
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1083 ...GAGACCCCAACGCC.....ACGCAGCCAGAACTCGCCCGAAGA 1123
347 pSerGluAspAsp...MetGlnAlaGlnAlaSerGlyGluAsnProAla 363
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1124 CCCCAGGAGTTCGGCCCTTGGAGAGCCCCGTGGGAGCGTGGCGCGC 1173
363 lalaLeuProGluAspAspGluValProGluAspThrGlnHisAspPro 379
    ::::: ||||| ||||| ||||| |||||
1174 AAATCCCAACCAACTGGCACATCCCTGATCCAGAGCGCGGAGCGCT 1223
380 AsnSerAspProAspTyrTyrAsnAspMetProAlaValIleProValG1 396
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1224 TACCATCCCGCGGACCCCGCAACATGAGGCTGATC..... 1262
396 uGlnThrThrLysSerSerAlaValSerMetProIlePheAlaIaP 413
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1263 .....GCCGGCGCGGTGGGCGGCACTTCTTGGCGAGCCC 1296
413 heValAlaCysAlaValAlaLeuValGlyLeuLeuValTrp 426
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1297 TGGTCAATTGC.....GGAATGTGTACTGG 1322
seq_name: gp_pat:107884
seq_documentation_block:

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```

LOCUS       107884               1594 bp               linear      PAT 02-DEC-1994
DEFINITION   Sequence 2 from Patent EP 0139416.
ACCESSION   107884
VERSION     107884.1  GI:5894401
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1594)
AUTHORS    Berman, P.W. and Lasky, L.A.
TITLE      Molecularly cloned diagnostic product and method of use
JOURNAL    Patent: EP 0139416-A2 2 02-MAY-1985;
FEATURES    location/Qualifiers
            source          1..1594
            /organism="unknown"
BASE COUNT   310 a      541 c      460 g      283 t
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alignment_scores:
    Quality: 199.00      Length: 497
    Ratio: 0.948      Gaps: 21
    Percent Similarity: 42.254      Percent Identity: 21.932
alignment_block:
    US-09-994-064-11 x 107884 ..
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54 TACCGACACACCGACGAMCC.....CTTAAGGGGAGGG 88
18 lLeuAsnLysHisMetAspCysGlyLysArgCysCysSerGlyAla 35
   ::::: ||||| ||||| ||||| |||||
89 GCCATTTCAGAGAGAGAGGGGTATACAAAGTCTCTTAAGAACAG 138
35 lAlaValPheThrLeuPheTrpThrCysValArgIleMetArgGluHis 50
   ::::: ||||| ||||| ||||| |||||
139 GGGTTAGGAGTTGTTGCGTCAT.....AAGCTCAGCGCCGACGACCA 182
51 .....IleCysPheValArgAs 56
183 ACTAACCCGATCATCACTTATCCTTAAGTCTCTTTTGTCGTGCGTTC 232
56 nAlaMetAspArgHisLeuPheLeuArgAsnAlaPheTrpThrIleValL 73
   ::::: ||||| ||||| ||||| |||||
233 CGGTATG..... 239
73 euleuSerSerPheAlaSerGlnSerThrAlaAlaValThrTyrAspTyr 89
   ::::: ||||| ||||| ||||| |||||
240 .....GGGGGGGCTCGCGCCAGGTTGGGGCCGTGATTTGTTGTCGTC 284
90 lIleLeuGlnArgArg..... 94
285 ATAGTGGGCTTCATGAGGTCGCGGCAATATGCTTGGCGGATGCTC 334
95 .....AlaL 96
335 TCTCAAGATGGCCGACCCCAATCGCTTTCGCGGCAAGACCTCCGCTCC 384
96 euAspAlaLeuThrIlePro.....Ala 103
385 TGGACCACTGACCGACCTCGGGGGGTCCGGCGCGTACCATCATCCAG 434
104 ValGlyProTyrAsnArgTyr.....Le 111
435 GCGGGCTTACCGAACCCTTCCAGGCCCGCCAGCCTCCGATCAGGTTTA 484
111 uThrArgValSerArgGlyCysAspValValGluLeuAsnProIleSer 128
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485 CCGCGGTGTGAGCGCGCTGCGCGACGCTGCTCTAAACGACCGCTGG 534

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ORIGIN

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alignment_scores:
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Quality:	198.00	Length:	342
Ratio:	1.215	Gaps:	15
Percent Similarity:	47.661	Percent Identity:	24.269

Percent Similarity: 47.661    Percent Identity: 24.269

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alignment_block:
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US-09-994-064-11 x E00395 . . .

Align seg 1/1 to: E00395 from: 1 to: 1594

[illegible]

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336 agLuseSeSgCluLyIsaLaPrOPrOGluAsSeSgLuAspasp...M 352
      |-----|-----|-----|-----|-----|
1097 C.....ACCCAGCCAAACATCGCCCGGGAAGACC CGGATTCGGCC 1140
      :::::
352 etGlnAlaGluAlaSeSgCluGluAsnPrOAlaAlaLeuPrOGluAspasp 368
      :::::
1141 TCATTGAGAGACCCCGTGGGAGCGGTGGCCGCCAAATCCCAACACTGG 1190
      :::::
369 GluValPrOGluAspThrGlnHisAspAspProAsnSerAspProAspTy 385
      :::::|-----|-----|-----|-----|
1191 CAATCCCGTCGATCCAGAGCGCCGACGCTTACCATCCCGGCCAC 1240
      :::::
385 rTyAsnAspMetPrOAlaValAlaPrOValGluGluThrThrLysSers 402
      :::::|-----|-----|-----|-----|
1241 CCGAACAACATGGCGCTGATC.....G 1263
      :::::
402 etAsnAlaValSerMetPrOILEPheAlaAlaPheValAlaCysAlaVal 418
      :::::|-----|-----|-----|-----|
1264 CCGCGCGGTGGGCGGCGCATGCTCTCGGACAGCCGCTCATTTGC..... 1307
      :::::
419 AlaLeuValGlyLeuLeuValTTP 426
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1308 .....GGAATTGTGTACTGG 1322

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seq\_name: gbb\_pat:E00401

seq\_documentation\_block:

LOCUS	E00401	1554 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	Herpes simplex virus-1 (HSV-1) glycoprotein D (gD) gene.				
ACCESSION	E00401				
VERSION	E00401.1	GI:2168684			
KEYWORDS	JP 1985155974-A/2.				
SOURCE	human herpesvirus 1.				

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FT TATA_signal 167. .171
FT /number=1 186. .191
FT TATA_signal
FT /number=2 1537. .1541
FT TATA_signal
FT /number=3 237. .116
FT mat_peptide /product='HSV-1 gD'
FT 237. .1419
FT CDS /product='HSV-1 gD'
FT

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FEATURES	Location/Qualifiers
source	1..1594
	/organism="human herpesvirus 1"
	/db_xref="taxon:10298"
BASE COUNT	308 a 542 c 461 g 283 t

## ORIGIN

## alignment\_scores:

Quality: 198.00 Length: 342  
Ratio: 1.215 Gaps: 15  
Percent Similarity: 47.661 Percent Identity: 24.269

## alignment\_block:

US-09-994-064-11 x E00401 ..

Align seg 1/1 to: E00401 from: 1 to: 1594

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101 lIleProAlaValAlGlyProTyrAsnArgTyrLeu..ThrArgValSerArg 117
    :::::::::: :::::::::: :::::::::: ::::::::::
452 GTTCACGCCCCCAGACCTCCGATCACGGTTACGGCTGTGGAGCGGG 501
    :::::::::: :::::::::: :::::::::: ::::::::::
117 LysAspValValAlGluLeuAsnProIleSerAsnValAspAspMetIle 133
    :::::::::: :::::::::: :::::::::: ::::::::::
502 CTTGCCCGAGCGGTGCTCTTAACGACCGCTGGAGGCCCGCCAGATTGTC 551
    :::::::::: :::::::::: :::::::::: ::::::::::
134 SerAlaAlaLysGluLysGluLysGlyLysProPheGluAlaSerVala 150
    :::::::::: :::::::::: :::::::::: ::::::::::
552 CGCGGGGCTCCGAAAGACGTCGGAAACACACCTACACACCTGACCATGCG 601
    :::::::::: :::::::::: :::::::::: ::::::::::
150 lTrpPheTyrValAlIleLysGlyAspAspGlyLysAspLysTyrCysProI 167
    :::::::::: :::::::::: :::::::::: ::::::::::
602 TTGGTTTCGGATG.....GGAGGCAACTGTGCTATGCCCA 636
    :::::::::: :::::::::: :::::::::: ::::::::::
167 lEtyArgLysGluTyrArgLysGlyAspValAlGluLeuSerGlu 183
    :::::::::: :::::::::: :::::::::: ::::::::::
637 TCACGGTATGAGTACACCGATCTCTTACACAACTCTGGGGGCC 686
    :::::::::: :::::::::: :::::::::: ::::::::::
184 CysAlaValAlGlnSerAlaGlnMetTrpAlaValAspTyrValProSer.. 199
    :::::::::: :::::::::: :::::::::: ::::::::::
687 TGTCACATCCGACGACGACCGCCGCTG.....AACTACTATGACAGCTT 730
    :::::::::: :::::::::: :::::::::: ::::::::::
200 ..ThleuValSerArgAsnGlyAlaGlyLeuThrIlePheSerProMra 216
    :::::::::: :::::::::: :::::::::: ::::::::::
731 CAGCGCTCGAGGAGATACCTGGGCTCTCTGTCAGACGCGCCCGGCT 780
    :::::::::: :::::::::: :::::::::: ::::::::::
216 lAlaLeuSerGlyLysIleTyrLeuLeuThrLeuLysIleGlyArgPheAla 232
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781 TTGAGACGCGCGGCGACGTACCTGGCGCTCGGAATTAACAGATGAGCG 830
    :::::::::: :::::::::: :::::::::: ::::::::::
233 GlnThrAlaLeuValThrLeuGlu.....ValAsnAspArgCysLeuLys 247
    :::::::::: :::::::::: :::::::::: ::::::::::
831 GAGATTACACAGATTATCTCTGAGCAGCAGCAGCAGGCGCTCCTGT...AA 877
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247 sIlleGlySerGlnLeuAsnPheLeuProSerLysCysTrpThrThrGluG 264
    :::::::::: :::::::::: :::::::::: ::::::::::
878 GTACACCTCCCGCTGGCGATCCCGCTGACGCTCTCTCCCGCCAGG 927
    :::::::::: :::::::::: :::::::::: ::::::::::
264 lNtyrGlnThrGly.....Phe 269
    :::::::::: :::::::::: :::::::::: ::::::::::
928 CCTACACAGAGGGGTGACGAGTGCAGACATCGGATGTCGCCCGCTTC 977
    :::::::::: :::::::::: :::::::::: ::::::::::
270 GlnGlyGlnHisLeuTyrProIleAlaAspThrAsnThrArgHisAlaAs 286
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978 ATCCCGGAGAACCGACGACGCTCGCTATACCTTGAAATATGCCGG 1027
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286 PaspAlaValArgLysGlyValAspIleLeuGlnArgTrpAsnAsnLeuL 303
    :::::::::: :::::::::: :::::::::: ::::::::::
1028 G.....TGGCAC..... 1034
    :::::::::: :::::::::: :::::::::: ::::::::::
303 euArgLysLysAsnProSerAlaProAspProArgProAspSerValPro 319
    :::::::::: :::::::::: :::::::::: ::::::::::
1035 .....GGGCCAGAGGCCCA...TACACGACACACCTGTGCC 1070
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320 GlnGluIleProAlaValThrLysLysAlaGluGlyArgTrpProAspAl 336
    :::::::::: :::::::::: :::::::::: ::::::::::
1071 CCGAGAGTGGCC.....GAGACCCCAACGCG 1096
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```

336 agLysSerGluLysLysAlaProProGluAspSerGluAspAsp...M 352
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1097 C.....ACGAGCCAGAACTCGCCCGGAGAACCCGAGAGATTGGGCC 1140
    :::::::::: :::::::::: :::::::::: ::::::::::
352 etGlnAlaGluAlaSerGlyLysAsnProAlaAlaLeuProGluAspAsp 368
    :::::::::: :::::::::: :::::::::: ::::::::::
1141 TCTTGAGAGAACCCCGTGGGACGCTGGCGCCGCAATCCACCAAACTGG 1190
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369 GluValProGluAspThrGlnHisAspAspProAsnSerAspProAspTyr 385
    :::::::::: :::::::::: :::::::::: ::::::::::
1191 CACATCCCTGCGATCCAGACGCCGCGACGCTTACCATTCGCCGCCAC 1240
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385 rTyrAsnAspMetProAlaValIleProValAlGluGluThrThrLysSer 402
    :::::::::: :::::::::: :::::::::: ::::::::::
1241 CCCGACAACTGGGCTGATC.....G 1263
    :::::::::: :::::::::: :::::::::: ::::::::::
402 eRAsnAlaValSerMetProIlePheAlaAlaPheValAlaCysAlaVal 418
    :::::::::: :::::::::: :::::::::: ::::::::::
1264 CGGCGCGGTGGCGGCGCATCTCTGCGACGCCCTGTCATTGTC..... 1307
    :::::::::: :::::::::: :::::::::: ::::::::::
419 AlAlaLeuValGlyLeuLeuValTrp 426
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1308 .....GGAATTGTACTGG 1322
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seq\_name: gb\_pat:100103

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seq_documentation_block:
LOCUS 100103 1608 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4891315.
ACCESSION 100103
VERSION 100103.1 GI:313953
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1608)
AUTHORS
Watson, R.J., Weis, J.H. and Engquist, L.W.
TITLE
Production of herpes simplex viral proteins
JOURNAL
Patent: US 4891315-A 1 02-JAN-1990;
American Cyanamid Company;
Stamford, CT
On Jul 30, 1993 this sequence version replaced gi:285497.
FEATURES
location/Qualifiers
1..1608
BASE COUNT 313 a 541 c 466 g 288 t
ORIGIN

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## alignment\_scores:

Quality: 197.50 Length: 498  
Ratio: 0.927 Gaps: 21  
Percent Similarity: 42.771 Percent Identity: 21.687

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US-09-994-064-11 x 100103 ..

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2 HisArgProHisLeuArgArgHisSerArgTyrTrpAlaLysGlyGluVal 18
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58 TACGACACACACCGACGAAAC.....CCTAAGGGGGAGG 92
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18 lLeuAsnLysHisMetAspCysGlyLysArgCysCysSerGlyAla 35
    :::::::::: :::::::::: :::::::::: ::::::::::
93 GCCATTTCACGAGGAGGAGGGGTATTAACAAGTCTGCTTTAAAGAGAG 142
    :::::::::: :::::::::: :::::::::: ::::::::::
35 lAlaValPheThrLeuPheThrCysValArgIleMetArgGluHis... 50
    :::::::::: :::::::::: :::::::::: ::::::::::
143 GGGTTAGGAGAGTGTTCGTCAT.....AAGCTTCACGCGGAGACGACGA 186
    :::::::::: :::::::::: :::::::::: ::::::::::
51 .....lIecysPheValArgAs 56
    :::::::::: :::::::::: :::::::::: ::::::::::

```

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187 ACTACCCGATCATGATTATCTTAAGGCTCTTTGTGTGGCTTC 236
56 nalmetasparghisleupheleuargasnalaiphetrptthilevall 73
237 CGGTATG..... 243
73 euleuserphealaserinserthrAlaIaValThrTyAspTyr 89
244 .....GGGGGAGCTGCCGAGGTTGGGGCCGCGATTTTGTGTGCTC 288
90 IleuGlyArgArg..... 94
289 ATAGTGGCTCCATGCGGGTCCCGGCAATATGCTTGGCGATGCTC 338
95 ..... 416 ALA 96
339 TCTCAAGATGGCCGACCCCAATGCTTTCGCGCAAGACCTTCCGCTCC 388
96 euaspalaleuThrIlePro.....Ala 103
389 TGGACCAAGTGCACCGACCTCCGGGGGTCGGCGCTGACCAATCCAG 438
104 ValGly.....ProTyrAsnArgTyr 110
439 GCGGGCTACCGGACCGCTTCCAGCCGCCAGCCCTCCGATCAGGCTTA 488
110 rleuThrArgValSerArgGlyCysAspValValGluLeuAspProIles 127
489 CTACGCGCTGTGGAGCGCGCTGCGCAGCGCTCTCTTAAGCAGCAGCG 538
127 eAsnValAspAspMetIleSerAlaIaLysGluLysGly 143
539 CGGAGGCCGCCGAGATTGTCGCGGGGCTCCGAAAGACGTCGGAACAA 588
144 ProPheGluAlaSerValValTrrpHeryValIleLysGlyAspAspI 160
589 CCTCAACACTGACATCGCTGTGTTGGATG.....GG 623
160 ygluAspLysTyrCysProIleTyrArgLysGluTyrArgGlyCysGly 177
624 AGGCAACTGTGTCATCCCATCAGCGGTCAAGTACACCGATGCTCTCT 673
177 spValGluLeuuserGluCysAlaValGluSerAlaGlnMetTrrpAla 193
674 ACAACAGTCTCTGGGGCTGTCCATCCGAGCGACGCCGCTGG... 720
194 ValAspTyrValProSer...ThrLeuValSerArgAsnGlyAlaGlyLe 209
721 ...AACTATATGACAGCTTCAAGCGCGTCAGCGAGATACCTGGGTT 767
209 uThrIlePheSerProThrAlaIaLeuSerGlyGlnTyrLeuLeuThrL 226
768 GGTGATGTCAGCGCCCGCTTGGAGACCGCGACGCTACGCGGCTCG 817
226 euLysIleGlyArgPheAlaGlnThrAlaLeuValThrLeu..... 240
818 TGAAGATTAACAGCTGAGGAGATTACACAGTTATCTTGAGCAGCA 867
241 ValAsnAspArgCysLeuLysIleGlySerGlnLeuAsnPheLeuProse 257
868 GCCAAGGGTCTCTGT...AAGTACGCCCTCCGCTGCGATCCGCCGCTC 914
257 rLysCysTrrpThrThrGluGlnTyrGlnThrGly..... 268
915 ACCCTGCTCTCTCCCGGAGCTTACAGCAGGGGGTGAGCGTGCAGCA 964
269 .....PheGlnGlyGlnHisLeuTyrProIleAlaAsp 279
965 TCGGAGTGTGCGCCGCTTCATCCCGAGAACCGACCGCGCGCTTA 1014
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1015 TACAGCTTAAGATCGCGGG..... 1035

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296 uGlnArgTrrpAsnAsnLeuLeuArgLysAsnProSerAlaProAsp 313
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1058 ACACGAGACACCTGCTGCCCCGAGACTG..... 1086
330 GluGlyArgThrProAspAlaGlnSerSerGluLysLysAlaProProG 346
1087 ...TCCGAGACCCCAAGCCG.....ACGACACGAACTCGCCCGGA 1127
346 uAspSerGluAspAsp...MetGlnAlaGluAlaSerGlyGluAsnPro 362
1128 AGACCCGAGGATTCGCTCTTGGAGAGCCCGTGGGAGCGTGGCCG 1177
362 lAlaLeuProGluAspAspGluValProGluAspThrGlnHisAspAsp 378
1178 CGCAATCCCAACCAACTGCGACATCCGTCGATCCAGAGCGCGGAGAG 1227
379 ProAsnSerAspProAspTyrTyrAsnAspMetProAlaValIlePro 395
1228 CCTTACCATCCCGCGCCACCCGCAACATGCGCTGATC..... 1269
395 lGluGluThrThrLysSerSerAsnAlaValSerMetProIlePheAla 412
1270 .....GCGGCGCGGTGGGCGGCGAGCTCTCTGCGAG 1300
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1301 CCTTGTCATTTC.....GGATTTGTGTACTG 1329

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LOCUS AR043518 1608 bp DNA Linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5814486.
ACCESSION AR043518
VERSION AR043518.1 GI:5964526
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1608)
AUTHORS Cohen, G.H., Eisenberg, R.T. and Nicola, A.
TITLE Herpes simplex virus glycoprotein D variants
JOURNAL Patent: US 5814486-A 3 29-SEP-1998;
FEATURES
SOURCE 1..1608
/organism="Unknown"
BASE COUNT 313 a 542 c 465 g 288 t
ORIGIN

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Quality: 193.50 Length: 498
Ratio: 0.908 Gaps: 21
Percent Similarity: 42.771 Percent Identity: 21.486

alignment_block:
US-09-994-064-11 x AR043518 ..
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2 HisArgProHisLeuArgArgHisSerArgTyrTrrpAlaLysGlyVal 18
58 TACGACCAACCGAGCAACC.....CTTAAGGGGAGAGG 92
18 lLeuAsnLysHisMetAspCysGlyGlyLysArgCysCysSerGlyAla 35
93 GCCATTTTACGAGAGGAGGGGATATACAAAGTCTCTTAAAGACAG 142

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35 laValaPheThrLeuPheThrPheCysValArgIleMetArgLys... 50
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143 GGGTAAAGGAGTGTTCGCTCAT.....AAGCTTCAGCGCGAAGACCA 186
51 .....11cysPheValArgAs 56
187 ACTACCCGATCATGATTATCCTTAAGGTCTTTTGTGTGTGCTGCTC 236
56 naIaMetAspArgHisLeuPheLeuArgnaIaPheThrPheValL 73
   ::|||
237 CGGTATG..... 243
73 euleuSerSerPheAlaSerGlnSerThrAlaAlaValThrTyraPyr 89
   ::|||::: ||::: ::
244 .....GGGGGAGCTGCGCCGAGGTTGGGGGCGGTATTTGTGTGCGTC 288
90 IleLeuGlyArgArg..... 94
289 ATAGTGGGCTTCATGGGGTCCGCGCAATATGCCCTTGGCGAGCCCTC 338
95 .....AlaL 96
339 TGTCAAGATGGCCGACCCCAATCGCTTCGGGGCAAGACCTCCGGTCC 388
96 euAspAlaLeuThrIlePro.....Ala 103
   ||||| ||||| ||
389 TGGACCACTGACCGACCCCTCCGGGGTCCGGCGGTACACATCCAG 438
104 ValGly.....ProTyraAsnArgTy 110
   ::|||
439 GCGGGCTTACCGGACCCGTTCCAGCCGCCCAAGCTCCGATCACGGTTA 488
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DEFINITION DNA sequence encoding gp-1 of herpes simplex virus typed.
ACCESSION E00204
VERSION E00204.1 GI:2168500
KEYWORDS JP 1984118097-A/1.
SOURCE human herpesvirus 1.
ORGANISM human herpesvirus 1.
REFERENCE 1 (bases 1 to 1608)
AUTHORS Rojlyaa,J.W., Jiyon,H.W. and Rln,u.E.
TITLE PRODUCTION OF HERPES SIMPLEX VIRUS PROTEIN
JOURNAL Patent: JP 1984118097-A 1 07-JUL-1984;
MORUKIYURAA JIENETETISUKUSU INC
OS Herpes simplex virus type 1
PN JP 1984118097-A/1
PD 07-JUL-1984
PF 20-JUL-1983 JP 198311151
PR 20-JUL-1982 US 82 400028, 25-OCT-1982 US 82 436368 PI
ROUJYAA JIYON MATOSON, JIYON HEINZU WAISU,
PI RAN UIRIMU ENKISUTO
PC C12P21/00,A61K39/245,C07G7/00,C07H21/04,C12N1/00,C12N15/00, PC
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PC C12R1:19), (C12N1/00,C12R1:19), (C12N1/00,C12R1:19): CC
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topology: Linear;
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CC anti-sense: No;
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DEFINITION Sequence 1 from Patent US 4762779.  
ACCESSION I01122  
VERSION I01122.1 GI:269313  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1608)  
TITLE Sultman, D. L.  
JOURNAL Compositions and methods for functionalizing nucleic acids  
Patent: US 4762779-A 1 09-AUG-1988;  
Amgen Inc.;  
Thousand Oaks, CA  
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1251 GTGCGGCTCGTGGGCTACTGTTGGAGCATGTAATAATCGCGCGCTTA 1300
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||
1301 GC 1302

seq_name: /SID1/gcdata/geneseq/geneseq-emb1/NA1995.DAT:AA133505
seq_documentation_block:
ID AA133505 standard; DNA; 1305 BP.
XX
AC AA133505;
XX
DT 19-NOV-1996 (first entry)
XX
DE Infectious laryngotracheitis virus gp gene.
XX
KW Infectious laryngotracheitis virus; ILTV; herpesvirus;
KW attenuation; vector; vaccine; chicken; poultry; immunisation;
KW glycoprotein gp; ds.
XX
OS Infectious laryngotracheitis virus.
XX
PN WO9508622-A1.
XX
PD 30-MAR-1995.
XX
PF 16-SEP-1994; 94MO-US10628.
XX
PR 24-SEP-1993; 93US-0126597.
XX
PA (SYTR ) SYNTRO CORP.
XX
PI Cochran MD, Wild MA;
XX
DR WPI: 1995-139591/18.
XX
P-PSDB: AAW00638.
XX
PT Recombinant attenuated infectious laryngotracheitis virus - for use
PT in vaccines to protect poultry from infection from the virus, also
PT methods of distinguishing between vaccinated and naturally infected
PT birds
XX
PS Example 1; Page 106-107; 177pp; English.
XX
CC The gd gene (AA133505) spans bases 8462-9766 of the unique short
CC region (see also AA133504) of infectious laryngotracheitis virus
CC (ILTV) genomic DNA. It codes for a glycoprotein (AAW00638) of
CC approx. 48,477 mol.wt. that is homologous to pseudorabies
CC virus g50 and to gd from herpes simplex virus-1. Marek's

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CC disease virus, IPV and bovine herpesvirus-1.1. Monoclonal  
 CC antibodies raised to ILTV react specifically with gp from  
 CC ILTV and also with ILTV gp expressed in herpesvirus of  
 CC turkeys (HVT) virus vector. ILTV gp expressed in the HVT  
 CC vector is useful as a subunit vaccine.  
 XX

SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

# alignment\_scores:

Quality: 2311.00 Length: 434  
 Ratio: 5.325 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

us-09-994-064-11 x AAT33505 ..

Align seg 1/1 to: AAT33505 from: 1 to: 1305

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51 GGTGCTTAACAACAACATGATGGATGGGTAAGAAACGGTCTCTCAGGCG 100
34 laAlaValPheThrLeuPheThrPheCysValArgIleMetArgGluHis 50
101 CAGCGATTCACCTCTTCTGAGACTGTGTCAGGATTAAGCGGAGCAT 150
51 IleCysPheValArgAsnAlaMetAspArgHISLeuPheLeuAArgAsnI 67
151 ATCTGCTTTGACGACGACGATAGGACCGCATTTATTTTGAGGAATGC 200
67 aPheThrThrIleValLeuLeuSerSerPheAlaSerGlnSerThrAlaA 84
201 TTTTGGACATTCGACTGCTTTCTCTCTCTGCTAGCCAGACACCGCG 250
84 laValThrTyraSPtyrIleLeuGlyArgArgAlaIleuAspAlaLeuThr 100
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101 IleProAlaValGlyProTyraSPtyrAsnArgTYrLeuThrArgValSerArgI 117
301 ATACCGGGGCTTGGCCGCTATTAACAGATACCTCCTAGGTATCAAGAG 350
117 yCysAspValValGluLeuAsnProIleSerAsnValAspAspMetIleS 134
351 CTGGACCTGTGAGCTCAACCCGATTTCTAACCTGGACGACATGATAT 400
134 eraIaAlaIalysGluLysGluLysGlyGlyProPheGluAlaSerValVal 150
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451 TGGTTCCTACGTATTAAGGGCGACGACGCGAGCAAGTACTGTCAT 500
167 eTYrArgLysGluTYrArgLysGluCysGlyAspValGlnLeuLeuSerGluC 184
501 CTATAGAAAGATGATGAGGATGGGACGCTCACTGCTATCTGATAT 550
184 ySaIaValGlnSerAlaGlnMetTrpAlaValAspTYrValProSerThr 200
551 GCGCGCTTCATCTGCACAGATGGGCGAGTGAGCTATGCTCTCAGAC 600
201 LeuValSerArgAsnGlyAlaGlyLeuThrIlePheSerProThrAlaI 217
601 CTGTATTCGCAAAATGGCGGCGACTGACTATATCTCCCCACACTGCTGC 650
217 aLeuSerGlyLysIleuLeuThrLeuLysIleGlyArgPheAlaGlnT 234
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701 CAGCTCTGTACTACTAGAAAGTTAAAGATCGCTGTTAAAGATCGGTCG 750
251 GlnLeuAsnPheLeuProSerLysCysTrpThrTrnGluGlnTYrGluTh 267
751 CAGCTTAACCTTTTACCGTGAATGCTGACACAGAAACAGATATCAGAC 800
267 rGlyPheGlnGlyGluHISLeuTYrProIleAlaSPtyrAsnThrArgH 284
801 TGGATTTCAGGCGAACAACACTTATTCGATCCGACACACATATACAGAC 850
284 lSaIaSPAspValTYrArgGlyTYrGluAspIleLeuGlnArgTrpAsn 300
851 ACGCGGACGACGTATATCGCGATACGAAGATATTCGACGCGCTGCAAT 900
301 AsnLeuLeuArgLysLysAsnProSerAlaProAspProArgProAspSe 317
901 AATTTGCTGAGGAAAGAAATCTTAGCGCGCCAGACCTCTCTCAGATAG 950
317 rValProGlnGluIleProAlaValThrLysLysAlaGluGlyArgThrP 334
951 CGTCCCGCAAGAAATTCCTCGCTTAACCAAGAAAGCGGAGGCGCACCC 1000
334 roAspAlaGlnSerSerGluLysLysAlaProProGluAspSerGluAsp 350
1001 CGGACGCGAAGAAAGCAGCGAAAGAGCCCTCCAGAAAGACTCGGAGGAC 1050
351 AspMetGlnAlaGluAlaSerGlyLysAsnProAlaIleAlaLeuProGlu 367
1051 GACATGCAAGGACAGAGCTTCTGAGAAATCTCGCCCTCCCGAAGA 1100
367 pAspGluValProGluAspThrGluHISAspAspProAsnSerAspProA 384
1101 CGAGCAAGTCCCGGAGACCGGACGACGATGATCCAAACTGGATCTCG 1150
384 sPTyTYrAsnAspMetProAlaValIleProValGluGluThrLys 400
1151 ACTATTACAAATGACATGCCCGCGTATCCCGTGAGAGACTACTAAA 1200
401 SerSerAsnAlaValSerMetProIlePheAlaIlePheValAlaCysAl 417
1201 AGTTCTAATGCGCTCCATGCGCAATATTCGGGGTTCGTAAGCTGCGC 1250
417 aValAlaLeuValGlyLeuLeuValTrpSerIleValLysCysAlaArgS 434
1251 GGTGCGCTCGTGGGGCTACTGTGTTGGAGCATCGTAAATGCGCGGTA 1300
434 er 434
1301 GC 1302
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seq_documentation_block:
ID AAX81152 standard; DNA: 1305 BP.
AC AAX81152:
XX
XX 07-SEP-1999 (first entry)
XX
XX Seq ID No: 19 of US5925358.
XX
XX Fowlpox virus; FPV, recombinant; vaccine; immunisation; chicken; NDV.
XX Newcastle disease virus; NDV, Fowlpox; Infectious laryngotracheitis; ds.
XX Fowlpox virus.
XX US5925358-A.
XX
XX 20-JUL-1999.
PD

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XX 07-JUN-1995; 95US-0484575.  
 PF  
 XX 07-JUN-1995; 95US-0484575.  
 PR 26-FEB-1993; 93US-0024156.  
 PR 28-FEB-1994; 94WO-US02252.  
 XX  
 PA (SYTR ) SYNPRO CORP.  
 PI Cochran MD, Junker DE.  
 DR WPI, 1999-418249/35.  
 DR P-PSDB; AAY21984.  
 XX  
 PS Fowlpox viruses, useful as vaccines for immunization of  
 PT chickens/turkeys against Fowlpox and Newcastle disease virus  
 XX  
 PS Disclosure; Columns 77-82; 108pp; English.  
 CC The invention relates to a recombinant fowlpox virus (FPV) comprising  
 CC a foreign DNA inserted into a region of the fowlpox virus genome  
 CC corresponding to a 2.8 kb EcoRI fragment, capable of being expressed in a  
 CC host cell. The virus is used as a vaccine for immunizing chickens against  
 CC Newcastle disease virus (NDV), Fowlpox, and Infectious Laryngotracheitis.  
 XX  
 SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;

## alignment\_scores:

Quality: 2311.00 Length: 434  
 Ratio: 5.325 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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 34 laaIaValPheThrLeuPheThrCysValArgIleMetArgGluHis 50  
 101 CAGCTGATTCACCTCTTCTGGACTGTGTGACAGATTATGCGGAGCAT 150  
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 201 TTTTGGACATGCTACTGCTTCTTCTTCCTGCTAGCCAGACGCCCGC 250  
 84 laValThrTyrAspTyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100  
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 101 IleProAlaValAlaGlyProTyrAsnArgTyrLeuThrArgValSerArgI 117  
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 501 CTATAGAAAGAGTACAGAGGATGTGGCGACGTACCAAGCTGCTGTAAT 550  
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 551 GCGCGTTCAATTCGACAGATGTGGCAGATGAGCTATGTTCTCAGACCC 600  
 201 LeuValSerArgAsnGlyAlaGlyLeuThrIlePheSerProThrAlaI 217  
 601 CTGTATCGCGAAATGGCGGGGACTGATATATTCCTCCCATGCTGC 650  
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 651 GCTCTCGGCCAATACTTGTGACACCTGAAATCGGAGATTTGCGGAAA 700  
 234 hralaLeuValThrLeuGluValAsnAspArgCysLeuLysIleGlySer 250  
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 334 roAspAlaGluSerSerGluLysLysAlaProProGluAspSerGluAsp 350  
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 1151 ACTATTACATGACATGCCCCGCGGTATCCCGGTGAGGAGACTACTAAA 1200  
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ID AAC67867 standard; DNA: 1305 BP.  
XX  
AC AAC67867;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Recombinant fowlpox virus-related polynucleotide. SEQ ID NO: 19.  
XX  
KW Fowlpox virus; FPV; antiviral; antibacterial; vaccine;  
KM Newcastle's disease; Marek's disease; infectious laryngotracheitis; ds.  
XX  
OS Unidentified.  
XX  
PN US6136318-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 07-JUN-1995; 95US-0486414.  
XX  
PR 26-FEB-1993; 93US-0024156.  
PR 28-FEB-1994; 94WO-US02252.  
XX  
PA (JUNK/) JUNKER D E.  
XX (COCH/) COCHRAN M D.  
XX Cochran MD, Junker DE;  
XX  
DR WPI: 2000-686071/67.  
XX  
PT New recombinant fowlpox virus useful as vaccines contains foreign DNA  
PT inserted into specific non-essential region of the genome  
XX  
PS Disclosure: Column 77-80; 56pp; English.  
XX  
CC The present sequence is provided in a specification relating to a  
CC recombinant fowlpox virus (FPV) that comprises a foreign DNA inserted  
CC within a 3.5 kb EcoRI fragment of the FPV genomic DNA. The foreign DNA  
CC can be expressed in host cells infected with FPV. The recombinant FPV  
CC may be used in vaccines to protect animals (especially chickens) against  
CC fowlpox and, depending on the source of the foreign DNA, other diseases,  
CC particularly Newcastle's disease, Marek's disease or infectious  
CC laryngotracheitis.  
XX  
SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;  
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Quality: 2311.00 Length: 434  
Ratio: 5.325 Gaps: 0  
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51 GGTGCTTAACAACAACATGATGCGGTGGAAGAAAGCGTCTGCTCAGCG 100  
34 lAlaValPheThrLeuPheThrPheCysValArgIleMetArgGlnHis 50  
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151 ATCTGCTTTGTACGCAACGCTATGAGCCGCCATTTATTTTGGAGAAATGC 200  
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84 lAlaIThrTyrAspTyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100  
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301 ATACCGGCGGTGGCCGTATACAGATACCTCACTAGGTATCAAGAGG 350  
117 yCysAspValValGlyLeuAsnProIleSerAsnValAspAspMetIle 134  
351 CTGGCAGCTGTGACGTCACCCGATTTCTACGTGAGCAGATGATAT 400  
134 eAlaAlaLysGlyLysGlyLysGlyProPheGlnAlaSerValVal 150  
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167 eTyrArgLysGlyTyrArgGlyCysGlyAspValGlnLeuLeuSerGlu 184  
501 CTATAGAAAGAGTACAGGGAATGTGGCAGCTCACTATCTCAT 550  
184 yAlaValGlnSerAlaGlnMetTrpAlaValAspTyrValProSerThr 200  
551 GCGCGCTTCAATCTGCACAGATGTGGCAGTGTGACTATGTTCTTACGACC 600  
201 LeuValSerArgAsnGlyAlaGlyLeuThrIlePheSerProThrAla 217  
601 CTGTATCGCAAAATGGCGGCGACTGACTATATTTCTCCCATGCTGCG 650  
217 aLeuSerGlyGlnTyrLeuLeuThrLeuLysIleGlyArgPheAlaGln 234  
651 GCTCTGCGCCAAATCTGTGACCTCGAATAATGGGAGATTGCGCAAA 700  
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751 CAGCTTAACCTTTTACCGTCGAAATGCTGAGCAACACAGACGATACAG 800  
267 rGlyPheGlnGlyLysIleLeuTyrProIleAlaAspThrAsnThrArg 284  
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301 AsnLeuLeuArgLysLysAsnProSerAlaProAspProArgProAsp 317  
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317 rValProGlnGlyIleProAlaValThrLysLysAlaGlnGlyArgThr 334  
951 CGTCCCAAGAAATATCCCGCTTAACCAAGAAAGCGAAGGCGCAGCC 1000  
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|||||
1151 ACTATTACATAGCATGCCCCGCGTATCCCGGTGAGGAGACTTACTATA 1200
401 SerSerAsnAlaValSerMetProIlePheAlaAlaPheValAlaCysAl 417
|||||
1201 AGTTCTTAAGCCGCTCCCAATGCCATATTCGCGGCTGTGAGCCCGCC 1250
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AC AAZ49300;
AT 14-MAR-2000 (first entry)
DE ILTV glycoprotein D (gd) gene.
KM Fowlpox virus; FPV; recombinant; antigenic protein; expression;
KM Infectious laryngotracheitis virus; ILTV; Newcastle disease virus; NDV;
KM Marek's disease virus; cytokerin; promoter; homologous recombination;
KM homology vector; multivalent; live vaccine; glycoprotein D; ds.
XX OS Infectious laryngotracheitis virus.
XX FH Key Location/Qualifiers
XX FT CDS 1..1305
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XX FT /product= "Glycoprotein D (gd)"
XX PN US6001369-A.
XX PD 14-DEC-1999.
XX PF 07-JUN-1995; 95US-0477459.
XX PR 26-FEB-1993; 93US-0024156.
XX PR 28-FEB-1994; 94MO-US02252.
XX PA (SYTR ) SYNTRO CORP.
XX PI Junker DE, Cochran MD;
XX WPI: 2000-071638/06.
XX DR P-PSDB: AAY58184.
XX PT Recombinant fowlpox virus useful as a vaccine for immunizing fowl
XX PT against Marek's disease, Newcastle disease, Infectious
XX PT Laryngotracheitis Virus and/or fowlpox
XX PS Claim 5: Columns 77-80; 56pp; English.
XX CC The invention relates to a recombinant fowlpox virus (FPV)
XX CC comprising a foreign DNA inserted into a 4.2 kb EcoRI fragment
XX CC of the fowlpox virus genome. The foreign DNA is capable of being
XX CC expressed in a host cell into which the fowlpox virus has been
XX CC introduced and encodes an antigenic protein. The antigenic protein
XX CC which may be expressed includes infectious laryngotracheitis virus
XX CC (ILTV) glycoprotein B (gB) or glycoprotein D (gD, AAY58184), Newcastle
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CC disease virus (NDV) haemagglutinin (HN, AAY58182) or fusion (F) protein
CC (AAY58183) and Marek's disease virus gB or gD. The foreign DNA may
CC alternatively encode a cytokine such as chicken myelomonocytic growth
CC factor (CMGF) or chicken interferon (cIFN). The foreign DNA in the
CC recombinant FPV is under the control of one or more synthetic pox
CC promoters, enabling control of strength and timing of heterologous
CC gene expression. The synthetic pox virus promoters that may be used are
CC based on promoters of the vaccinia virus and include early promoter 1
CC (EP1), late promoter 1 (LP1), EP2 and LP2 (AAZ49291-249294,
CC respectively). The recombinant FPV is generated via homologous
CC recombination between FPV DNA and a homology vector containing the
CC foreign DNA flanked by FPV sequences. The recombinant fowlpox viruses of
CC the invention are used as multivalent live vaccines for immunising fowl
CC against Marek's disease virus, NDV, ILTV and/or fowlpox virus. The
CC present sequence represents the ILTV glycoprotein D (gd) gene.
XX SQ Sequence 1305 BP; 331 A; 349 C; 344 G; 281 T; 0 other;
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alignment_scores:
Quality: 2311.00 Length: 434
Ratio: 5.325 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-994-064-11 x AAZ49300 ..
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|||||
151 ATCTGCTTTGTACGCAACGCTATGACCGCGCTGCTGCGCGCTAAC 200
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|||||
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84 laValThrTyrAspTyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100
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251 CCGTCACGTAAGTACATTTAGGCGCGCGCTGCTGCGCGCTAAC 300
101 IleProAlaValGlyProTyrAsnArgTyrLeuThrArgValSerArgG 117
|||||
301 ATACCGCGGCTTGCCCGTATAACAGATACCTCAGTAGGATATCAAGAG 350
117 yCysAspValIleGluAsnProIleSerAsnValAspAspMetIleS 134
|||||
351 CTGCGAGCTTGTGAGCTCAACCGATTTCTAAGTGAGAGACATGATAT 400
134 erAlaIleValGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 150
|||||
401 CGGCGCGCAAAAGAAAAAGAGAGGCGGCGCTTTCGAGCGCTCCGTC 450
151 ThrPheThrValIleLysGlyLysGlyLysGlyLysGlyLysGlyLys 167
|||||
451 TGGTCTACGCTGATTAAGGCGAGCGAGCGGAGAGACAGACTGCTCAAT 500
167 eTyrArgLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 184
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501 CTATAGAAAAGATACAGGAGATGTCGACGATCAACCTCTATCGAAT 550
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seq_documentation_block:
ID   AAT33504 standard; DNA; 13473 bp.
XX
XX   AAT33504;
XX
XX
XX   18-NOV-1996 (first entry)
XX
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DE	Infectious laryngotracheitis virus short region sequence.
XX	
KW	Infectious laryngotracheitis virus; ILTV; herpesvirus;
KW	attenuation; vector; vaccine; chicken; poultry; immunisation; ds
XX	
OS	Infectious laryngotracheitis virus.
XX	
FH	Key
FT	repeat_region
FT	/location/Qualifiers
FT	1..273
FT	*tag= a
FT	/function= internal repeat region
FT	274..13371
FT	*tag= b
FT	/function= unique short sequence of ILTV
FT	complement (281..970)
FT	*tag= c
FT	/label= US2_gene
FT	1059..2489
FT	*tag= d
FT	/label= Protein-kinase_gene
FT	2575..4107
FT	*tag= e
FT	/label= U147-like_gene
FT	4113..4445
FT	*tag= f
FT	/label= ORF4
FT	complement (4139..4519)
FT	*tag= g
FT	/label= ORF4_reverse_complement
FT	misc_difference 4535
FT	*tag= h
FT	/note= "base 4535 is given as 's' in the
FT	specification"
FT	4609..5487
FT	*tag= i
FT	/label= gG_gene
FT	5697..8654
FT	*tag= j
FT	/label= g60_gene
FT	complement (6948..7826)
FT	*tag= k
FT	/label= ORF6_reverse_complement
FT	8462..9766
FT	*tag= l
FT	/label= gD_gene
FT	9874..10962
FT	*tag= m
FT	/label= gI_gene
FT	complement (10617..11150)
FT	*tag= n
FT	/label= ORF8_reverse_complement
FT	11159..12658
FT	*tag= o
FT	/label= gE_gene
FT	12665..13447
FT	*tag= p
FT	/label= ORF10
FT	misc_difference 13002..13003
FT	*tag= q
FT	/note= "bases 13002-13303 are given as 'ss' in
FT	the specification"
FT	13372..13473
FT	*tag= r
FT	/function= terminal repeat region
XX	
XX	WO9508622-A1.
XX	
PN	30-MAR-1995.
PD	
PE	16-SEP-1994.
XX	94MO-US10628.
XX	
ER	24-SEP-1993.
XX	93US-0126597.
XX	

PA (SYTR ) SYNTRO CORP.  
 XX  
 PI Cochran MD, Wild MA:  
 XX  
 DR WPI: 1995-139591/18.  
 P-PSDB: AAM00630, AAM00631, AAM00632, AAM00633, AAM00634, AAM00635,  
 DR AAM00636, AAM00637, AAM00638, AAM00639, AAM00640, AAM00641 W00642.  
 XX  
 PT Recombinant attenuated infectious laryngotracheitis virus - for use  
 in vaccines to protect poultry from infection from the virus, also  
 PT methods of distinguishing between vaccinated and naturally infected  
 PT birds  
 XX  
 PS Example 1; Page 79-94; 177pp; English.  
 XX  
 CC The unique short region (AAT33504) of infectious laryngotracheitis  
 CC virus (ILTV) genomic DNA contains genes (see also AAT33505 and  
 CC AAT33510-13) that are associated with ILTV virulence. A deletion in  
 CC those genes, esp. the glycoprotein g6 gene, glycoprotein g1 gene,  
 CC thymidine kinase gene, US2 gene, UL47-like gene or the glycoprotein  
 CC g60 gene, will attenuate the ILTV. A gene for a foreign antigen may  
 CC be inserted into the US2, UL47-like, ORF4, g6, g60 or g1 gene to  
 CC produce a recombinant ILTV. Recombinant ILTV may be used as a  
 CC multivalent vaccine, esp. for use in poultry.  
 CC  
 XX Sequence 13473 BP; 3390 A; 3582 C; 3547 G; 2951 T; 3 other:  
 SQ

alignment\_scores:  
 Quality: 2311.00 Length: 434  
 Ratio: 5.325 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-994-064-11 x AAT33504 ..

Align seg 1/1 to: AAT33504 from: 1 to: 13473

1 MethisArProHISLeuArGArGHisSerArGTYrAlaLysGlyI 17  
 |||||||  
 8462 ATGCACCGCTCCATCTCAGACGCGACTCGCTTACTACGCCAAGAGAGA 8511  
 17 uValLeuAnLysHISMetAspCysGlyGlyLysArgCysSerGlyA 34  
 |||||||  
 8512 GGTGCTTAACAACACATGATGCGGTGGAACAGGTGCTGCTAGGCG 8561  
 34 laAlaValPheThrLeuPheThrPheCysValArgIleMetArgLuhis 50  
 |||||||  
 8562 CAGCTGATTCACCTCTTCTTGCACTTGTCAGAGATTATGGGGAGCAT 8611  
 51 IleCysPheValArgAsnAlaMetAspArgHISLeuPheLeuArgAsnAl 67  
 |||||||  
 8612 ATCTGCTTTGTACGCAACGCTATGACGCGCATTTATTTTTCAGGAATGC 8661  
 67 aPheThrPheIleValLeuLeuSerSerPheAlaSerGlnSerThrAlaA 84  
 |||||||  
 8662 TTTTGGACTATGCTACTGCTTCTTCTCTGCTGCAACAGACAGCGCG 8711  
 84 laValThrTyraSPtyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100  
 |||||||  
 8712 CCGTCACGTACGACTACATTTTAAAGCCGCGCGCTGACCGCTAAC 8761  
 101 IleProAlaValGlyProTyrAsnArgTyrIleuThrArgValSerArgI 117  
 |||||||  
 8762 AATACCGCGCGTGGCCCTATTAACAGATACCTCCTAGGATCAAGAGG 8811  
 117 yCysAspValValGluLeuAsnProIleSerAsnValAspAspMetIles 134  
 |||||||  
 8812 CTGCGACGTGTGCGAGCTCAACCCGATTCTTAACGTGAGCAGCATGATAT 8861  
 134 eValAlaLysGluLysGluLysGlyGlyProPheGluAlaSerValVal 150  
 |||||||  
 8862 CGCGCGCCAAAGAAAGAGAGGGGGCCCTTTGAGGCGCTCCGTCGTC 8911

151 TrpPheTyrValIleLysGlyAspAspCysGlyAspLysTyrCysProI 167  
 |||||||  
 8912 TGGTTCTACGTGATTAAAGGCGACGAGCGCGAGCAAGACTGTCAT 8961  
 167 eTyrArgLysGluTyrArgGluCysGlyAspValGlnLeuLeuSerGluC 184  
 |||||||  
 8962 CTATAGAAAAGACTACAGGAATGTGGCGACGTACACGTATCTGAAAT 9011  
 184 yAlaValGlnSerAlaGlnMetTrrPalValAlaSPtyrValProSerThr 200  
 |||||||  
 9012 GCGCCGCTCAATCTGCACAGATGTGGCGGTGACTATGTTCTTGACCC 9061  
 201 LeuValSerArgAsnGluValGluLeuThrIlePheSerProThrAlaI 217  
 |||||||  
 9062 CTTGTATCCGAAATGCGCGGACTGACTATATTTCTCCCCACATGCTGC 9111  
 217 aLeuSerGlyGlnTyrLeuLeuThrLeuLysIleGlyArgPheAlaGlnT 234  
 |||||||  
 9112 GCTCTGGCCATATCTGCTGACCTGAAATCGGAGATTTGGCGCAA 9161  
 234 hrAlaLeuValThrLeuGluValAsnAspArgCysLeuLysIleGlySer 250  
 |||||||  
 9162 CAGCTCTGTAACCTTAAGATTAAAGATCGCTTTAAAGATCGGCTCG 9211  
 251 GlnLeuAsnPheLeuProSerLysCysTrpThrThrGluGlnTyrGlnTh 267  
 |||||||  
 9212 CAGCTTACTTTTACCGTCGAATGCTGACACAGAACAGATATCAGAC 9261  
 267 rGlyPheGlnGlyLuhISLeuTyrProIleAlaSPThrAsnThrArgH 284  
 |||||||  
 9262 TGGATTTCAAGGCGCAACCTTTATCCGATCGCAGACCAACAAATACAGC 9311  
 284 IsAlaAspAspValTyrArgGlyTyrGluAspIleLeuGlnArgTrrPa 300  
 |||||||  
 9312 ACCGGACGACGATATCGGGGATACGAAGATTTCTGACGCCCTGGAA 9361  
 301 AsnLeuLeuArgLysLysAsnProSerAlaProAspProArgProAsp 317  
 |||||||  
 9362 AATTTGCTGAGAAAAGAAATCCTAGCGCCGACAGCCCTGCTCAATAG 9411  
 317 rValProGlnGluIleProAlaValThrLysLysAlaGluGlyArgThr 334  
 |||||||  
 9412 CGTCCCGCAAGAAATTCCTGCTTAACCAAGAAAGCGAGGCGCAGACC 9461  
 334 roAspAlaGlnSerSerGluLysLysAlaProProGluAspSerGluAsp 350  
 |||||||  
 9462 CGGACGCAAGAGCAGCGAAAGAGGCCCTCCAGAAAGACTGGAGGAC 9511  
 351 AspMetGlnAlaGluAlaSerGlyLysAsnProAlaAlaLeuProGluAs 367  
 |||||||  
 9512 GACATGACGAGGAGAGGCTCTGAGAAATCTGCCCTCCCTCCCGAGAG 9561  
 367 PASpGluValProGluAspThrGluHISAspAspProAsnSerAspPro 384  
 |||||||  
 9562 CGAGGAAGTCCCGAGAGACCGAGCAGATGATCAAACTCGGATCTG 9611  
 384 SPtyrTyrAsnAspMetProAlaValIleProValGluGluThrThrLys 400  
 |||||||  
 9612 ACTATTACAATGACATGCCCGCGCTGATCCGGTGGAGGAGACTACTAAA 9661  
 401 SerSerAsnAlaValSerMetProIlePheAlaAlaPheValAlaCysAl 417  
 |||||||  
 9662 AGTCTTAATGCCGCTCATGCCCATTATGCGGGCGTTCTGAGCTCGC 9711  
 417 aValAlaLeuValGlyLeuLeuValTrpSerIleValLysCysAlaArg 434  
 |||||||  
 9712 GGTGCGCTCTGGGGCTACTGTTGGAGCATGTTAAATGGCGGGGTA 9761  
 434 er 434  
 ||  
 9762 GC 9763

seq_name:	/SD15/gcgdata/geneseq/geneseqn-emb1/NA1596.DAT:AA144384
seq_documentation_block:	
ID	AA144384 standard; DNA: 13473 BP.
XX	
AC	AA144384;
XX	
DT	02-JUN-1997 (first entry)
XX	
DE	Infectious laryngotracheitis virus unique short region.
XX	
KM	ILTV: vaccine; vector: attenuation; poultry;
KM	avian infectious bronchitis virus; Newcastle disease virus;
KM	Infectious bursal disease virus of chickens;
KM	Marek's disease virus; herpesvirus; ss.
XX	
OS	Infectious laryngotracheitis virus USDA strain 8302.
XX	
FH	Key
FH	Location/Qualifiers
FT	repeat_region
FT	1..273
FT	/*tag= a
FT	274..13371
FT	/*tag= b
FT	/note="unique short region"
FT	161..166
FT	/*tag= c
FT	/note="polyA signal for ORF1"
FT	complement (281..970)
FT	/*tag= d
FT	/label="ORF1(RC)
FT	/note="unique-like short 2 (US2) gene"
FT	1007..1010
FT	/*tag= e
FT	/note="TATA signal for ORF1 and ORF2"
FT	1040..1043
FT	/*tag= f
FT	/note="TATA signal for ORF1"
FT	1042..1045
FT	/*tag= g
FT	/note="TATA signal for ORF2"
FT	1059..2489
FT	/*tag= h
FT	/label="ORF2
FT	/note="protein kinase gene"
FT	2491..2496
FT	/*tag= i
FT	/note="polyA signal for ORF2"
FT	2538..2543
FT	/*tag= j
FT	/note="polyA signal for ORF2"
FT	2575..4107
FT	/*tag= k
FT	/label="ORF3
FT	/note="unique long 47 (UL47)-like gene"
FT	4523..4526
FT	/*tag= l
FT	/note="TATA signal for ORF4"
FT	4113..4445
FT	/*tag= m
FT	/label="ORF4
FT	complement (4139..4519)
FT	/*tag= n
FT	/label="ORF4(RC)
FT	4523..4526
FT	/*tag= o
FT	/note="TATA signal for ORF5"
FT	4609..5487
FT	/*tag= p
FT	/label="ORF5
FT	/note="glycoprotein gg gene"
FT	4609..4686
FT	/*tag= q
FT	4687..5484
FT	mat_peptide

FT		/*tag= r
FT	polyA_signal	5564..5569
FT		/*tag= s
FT		/note= "polyA site for ORF5"
FT	polyA_signal	5653..5658
FT		/*tag= t
FT		/note= "polyA signal for ORF5"
FT	CDS	5697..8634
FT		/*tag= u
FT		/label= ORF6
FT	repeat_region	/note= "glycoprotein g60 gene"
FT		6987..7727
FT		/*tag= v
FT		/note= "repeat region consists of approx. 23
FT		repeats of 30-36 bp"
FT	CDS	complement (6948..7826)
FT		/*tag= w
FT		/label= ORF6(RC)
FT	TATA_signal	8455..8458
FT		/*tag= x
FT		/note= "potential TATA signal for ORF7"
FT	CDS	8461..9766
FT		/*tag= y
FT		/label= ORF7
FT		/note= "glycoprotein gD gene, alternative start
FT		codon at 8633..8635"
FT	TATA_signal	9819..9822
FT		/*tag= z
FT		/note= "TATA signal for ORF8"
FT	CDS	9874..10962
FT		/*tag= aa
FT		/label= ORF8
FT		/note= "glycoprotein gI gene"
FT	sig_peptide	9874..9939
FT		/*tag= ab
FT	mat_peptide	9940..10959
FT		/*tag= ac
FT		/note= "complement (10617..11150)
FT	CDS	/*tag= ad
FT		/label= ORF8(RC)
FT	TATA_signal	11069..11072
FT		/*tag= ae
FT		/note= "TATA signal for ORF9"
FT	CDS	11159..12658
FT		/*tag= af
FT		/label= ORF9
FT		/note= "glycoprotein gE gene"
FT	sig_peptide	11159..11212
FT		/*tag= ag
FT	mat_peptide	11213..12655
FT		/*tag= ah
FT	TATA_signal	12483..12486
FT		/*tag= ai
FT		/note= "TATA signal for ORF10"
FT	CDS	12665..13447
FT		/*tag= aj
FT		/label= ORF10
FT	repeat_region	13372..13743
FT		/*tag= ak
XX		
XX	PN	WO9629396-A1.
XX	PD	26-SEP-1996.
XX	PR	21-MAR-1996;
XX		96WO-US03916.
XX	PR	06-JUN-1995;
XX	PR	23-MAR-1995;
XX		95US-0468190.
XX		95US-0410121.
XX		(SYTR ) SYNTRO CORP.
XX	PI	Cochran MD, Wild MA;

DR WPI: 1996-443172/44.  
DR P-PSDB: AAM06782;  
DR P-PSDB: AAM06783;  
DR P-PSDB: AAM06784;  
DR P-PSDB: AAM06785;  
DR P-PSDB: AAM06786;  
DR P-PSDB: AAM06787;  
DR P-PSDB: AAM06788;  
DR P-PSDB: AAM06789;  
DR P-PSDB: AAM06790;  
DR P-PSDB: AAM06791;  
DR P-PSDB: AAM06792;  
DR P-PSDB: AAM06793.  
XX  
PT Recombinant infectious laryngotracheitis virus with deletion in the  
PT glycoprotein G, g1 or US2 gene, etc. - useful for vaccines against  
PT infectious laryngotracheitis in poultry  
XX  
PS Example 11: Page 88-103; 216pp; English.  
XX  
CC The nucleotide sequence of 13,473 bp of contiguous DNA (AAT44384)  
CC from the unique short region of infectious laryngotracheitis virus  
CC (ILT) contains the entire 13,098 bp unique short region and  
CC includes 13 open reading frames that encode proteins (AAM06782-94) of  
CC over 100 amino acids, 8 of which show significant homology to other  
CC virus genes. Novel recombinant, attenuated ILTV complements the ILTV  
CC genome contg. a deletion in the unique short region, esp. in the  
CC glycoprotein g6, g1, US2, ORF4, UL47-like or g60 gene. The  
CC attenuated virus is useful as a vaccine against ILTV. A foreign  
CC gene encoding an antigen e.g. from another avian virus can be  
CC inserted into the US2, UL47-like, ORF4, g6, g60 or g1 gene to  
CC provide a multivalent vaccine for chickens and other poultry.  
CC Deletion of the g6 or g1 gene provides as a negative marker to  
CC distinguish vaccinated from infected animals.  
XX  
SQ Sequence 13473 BP; 3390 A; 3581 C; 3547 G; 2952 T; 3 other:  
  
alignment\_scores:  
Quality: 2311.00 Length: 434  
Ratio: 5.325 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000  
  
alignment\_block:  
US-09-994-064-11 x AAT44384 ..  
  
Align seg 1/1 to: AAT44384 from: 1 to: 13473  
  
1 MethiAArgProHisLeuAArgHisSerArgTyrTyrAlaLysGlyI 17  
|||||  
8462 ATGCACGCTCATCTCAGACGCGACTCGCTACTACGCGAAGAGA 8511  
17 vAlleuAsnLysHisMetAspGlyGlyLysArgGlyCysSerLys 34  
|||||  
8512 GGTCCTTAACAAACACATGGATTGGCGGGAACCGTGCTGCACAGCG 8561  
34 laAlaValPheThrLeuPheTrpThrCysValArgIleMetArgGlnHis 50  
|||||  
8562 CAGCTGATTCACCTCTTTCTGCACTTGTCAGATTATGCGGAGCAT 8611  
51 IleCysPheValArgAsnAlaMetAspArgHisLeuPheLeuArgAsnAl 67  
|||||  
8612 ATCTGCTTTTACGCAACGCTATGACCGCATTTATTTTGAAGATGC 8661  
67 aPheTrpThrIleValLeuLeuSerSerPheAlaSerGlnSerThrAla 84  
|||||  
8662 TTTTGTGACATGCTACTGCTTCTTCCTTCGCTAGCCAGACGCCCG 8711  
84 laValThrTyrAspTyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100  
|||||  
8712 CCGTCAACGATGACTACATTTTAGCGCGCTGCGCGCTGACGCGCTAAC 8761  
101 IleProAlaValGlyProTyrAsnArgTyrLeuThrArgValSerArgI 117

|||||  
8762 ATACCGCGGCTTGCCCGCTATTAACAGATACCTCACTAGGGATCAACAGG 8811  
117 yCysAspValValGlyLeuLeuAsnProIleSerAsnValAspAspMetIle 134  
|||||  
8812 CTGCGACGTTGTGAGCTCAACCCGATTTCTAACGTGAGCAGCATGATAT 8861  
134 erAlaAlaLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 150  
|||||  
8862 CGCGGCCCAAGAAAGAGAGAGGGGGCCCTTTCGAGGCTCCGCTGC 8911  
151 TrpPheTyrValIleLysGlyAspAspGlyLysAspTyrCysProIle 167  
|||||  
8912 TGGTTCACGTGATTAGGGCGACGAGCGGAGGACAAAGTACTGTCCAAAT 8961  
167 eTyrArgLysGlyLysTyrArgGlyLysGlyAspValGlyLeuLeuSerLys 184  
|||||  
8962 CTATAGAAAGAGATACAGGAGATGTGGCAGCTACCACTCTATCTGAAT 9011  
184 yAlaValGlnSerAlaGlnMetTrpAlaValAspTyrValProSerThr 200  
|||||  
9012 GCGCGCTTCATCTGCACAGATGTGGCAGTGCATATGTTCTTCTAGCACC 9061  
201 LeuValSerArgAsnGlyAlaGlyLeuThrIlePheSerProThrAlaAl 217  
|||||  
9062 CTGTGATCGGGAATAGCGCGGAGCTGACTATATCTCCCCACCTGCTGC 9111  
217 aLeuSerGlyGlnTyrLeuLeuThrLeuLysIleGlyArgPheAlaLys 234  
|||||  
9112 GCCTCTGGCCCAATCTTGCTGACCCCGAAATCGGAGATTTGCGCAA 9161  
234 hrAlaLeuValThrLeuGlyValAsnAspArgCysLeuLysIleGlySer 250  
|||||  
9162 CAGCTCTCGTAACTCTGAAAGTTACGATCGCTTTTAAAGATCGGCTCG 9211  
251 GlnLeuAsnPheLeuProSerLysCysTrpThrThrGlnGlnTyrGlnThr 267  
|||||  
9212 CAGCTTAACCTTTTACCGTCGAAATGCTGGACAACAGACAGTATCAGAC 9261  
267 rgLysPheGlnGlyLysHisLeuTyrProIleAlaAspThrAsnThrArg 284  
|||||  
9262 TGGATTTCAGGCGAACACCTTTATCCGATCGCAGACCAACAAATACAGAC 9311  
284 IsAlaAspAspValTyrArgGlyTyrGlnAspIleLeuGlnArgTyrPasn 300  
|||||  
9312 ACCGCGACAGCATATATCGGGGATACGAAAGATATTCGACGCGTGAAT 9361  
9362 AATTGCTGAGAAAGAAAGAAATCCATGACGCGCCAGACCCCTGTCAGATAG 9411  
317 rValProGlnGlyIleProAlaValThrLysLysAlaGlyLysArgThrP 334  
|||||  
9412 CGTCCCGCAAGAAATTCCTCGTAAACCAAGAAAGGAGGCGCACCC 9461  
334 roAspAlaGlnSerSerGlyLysLysAlaProProGlnAspSerGlyAsp 350  
|||||  
9462 CGGACGCGAAGAGAGCGAAGAAAGAGCCCTCCAGAAAGACTCGGAGAGC 9511  
351 AspMetGlnAlaGlyLysArgGlyLysAsnProAlaAlaLeuProGlnLys 367  
|||||  
9512 GACATGACGACAGAGGCTTCTGAGAAATCTGCCCCCTCCCGCAGAGA 9561  
367 PaSPGlyValProGlnAspThrGlnHisAspAspProAsnSerAspPro 384  
|||||  
9562 CGAGGAAGTCCCGAGGACACCGAGCAGATGATCCAACTCGGATCTCG 9611  
384 sPtyrTyrAsnAspMetProAlaValIleProValGlnGlyLysThrLys 400  
|||||  
9612 ACTATTCAATGACATGCCCGCGTATCCCGGAGGAGACTACTAA 9661  
401 SerSerAsnAlaValSerMetProIlePheAlaAlaPheValAlaCysAl 417  
|||||

```
9662 AGTTCTAATGCCGTCTCCATGCCCATATTCGCGCGCTTCGTAGCCGCGC 9711
417 AValAlaIleuValGlyLeuValITrpSerIleValIlyscysAlaArgS 434
9712 GGTGGCGCTCTGTGGGCTACTGTGTTGGAGCATCGTAATAAGCGCGCGCTA 9761
434 er 434
9762 GC 9763

seq_name: /SIDSI/gcgdata/geneseq/geneseq-n-emb1/NA1996.DAT:AAAT44385
seq_documentation_block:
ID   AAAT44385 standard; DNM: 18912 BP.
XX   AAAT44385;
AC
XX   02-JUN-1997 (first entry)
XX
DE   Infectious laryngotracheitis virus unique short + flanking region.
XX
KW   ILRV; vaccine; vector; attenuation; poultry;
KW   avian infectious bronchitis virus; Newcastle disease virus;
KW   infectious bursal disease virus of chickens;
KW   Marek's disease virus; herpesvirus; ss.
XX
OS   Infectious laryngotracheitis virus USDA strain 8302.
XX
FH   Key Location/Qualifiers
FT   repeat_region 1..2909
FT   /tag= a
FT   /note= "short repeat region"
FT   697..1533
FT   /tag= b
FT   /label= "SRORF2"
FT   /note= "US10 gene"
FT   complement (2916..3605)
FT   /tag= c
FT   /label= "SKORF1"
FT   /note= "short repeat open reading frame 1"
FT   2910..16003
FT   /tag= d
FT   /note= "unique short region"
FT   2796..2891
FT   /tag= e
FT   /note= "polyA signal for ORF1"
FT   complement (2916..3605)
FT   /tag= f
FT   /label= "ORF1(RC)"
FT   /note= "unique-like short 2 (US2) gene"
FT   3642..3645
FT   /tag= g
FT   /note= "TATA signal for ORF1 and ORF2"
FT   3675..3678
FT   /tag= h
FT   /note= "TATA signal for ORF1"
FT   3677..3680
FT   /tag= i
FT   /note= "TATA signal for ORF2"
FT   3694..5124
FT   /tag= j
FT   /label= "ORF2"
FT   /note= "protein kinase gene"
FT   5126..5131
FT   /tag= k
FT   /note= "polyA signal for ORF2"
FT   5173..5178
FT   /tag= l
FT   /note= "polyA signal for ORF2"
FT   5210..7081
FT   /tag= m
FT   /label= "ORF3"
FT   /note= "unique long 47 (UL47)-like gene"

417 AValAlaIleuValGlyLeuValITrpSerIleValIlyscysAlaArgS 434
9712 GGTGGCGCTCTGTGGGCTACTGTGTTGGAGCATCGTAATAAGCGCGCGCTA 9761
434 er 434
9762 GC 9763

seq_name: /SIDSI/gcgdata/geneseq/geneseq-n-emb1/NA1996.DAT:AAAT44385
seq_documentation_block:
ID   AAAT44385 standard; DNM: 18912 BP.
XX   AAAT44385;
AC
XX   02-JUN-1997 (first entry)
XX
DE   Infectious laryngotracheitis virus unique short + flanking region.
XX
KW   ILRV; vaccine; vector; attenuation; poultry;
KW   avian infectious bronchitis virus; Newcastle disease virus;
KW   infectious bursal disease virus of chickens;
KW   Marek's disease virus; herpesvirus; ss.
XX
OS   Infectious laryngotracheitis virus USDA strain 8302.
XX
FH   Key Location/Qualifiers
FT   repeat_region 1..2909
FT   /tag= a
FT   /note= "short repeat region"
FT   697..1533
FT   /tag= b
FT   /label= "SRORF2"
FT   /note= "US10 gene"
FT   complement (2916..3605)
FT   /tag= c
FT   /label= "SKORF1"
FT   /note= "short repeat open reading frame 1"
FT   2910..16003
FT   /tag= d
FT   /note= "unique short region"
FT   2796..2891
FT   /tag= e
FT   /note= "polyA signal for ORF1"
FT   complement (2916..3605)
FT   /tag= f
FT   /label= "ORF1(RC)"
FT   /note= "unique-like short 2 (US2) gene"
FT   3642..3645
FT   /tag= g
FT   /note= "TATA signal for ORF1 and ORF2"
FT   3675..3678
FT   /tag= h
FT   /note= "TATA signal for ORF1"
FT   3677..3680
FT   /tag= i
FT   /note= "TATA signal for ORF2"
FT   3694..5124
FT   /tag= j
FT   /label= "ORF2"
FT   /note= "protein kinase gene"
FT   5126..5131
FT   /tag= k
FT   /note= "polyA signal for ORF2"
FT   5173..5178
FT   /tag= l
FT   /note= "polyA signal for ORF2"
FT   5210..7081
FT   /tag= m
FT   /label= "ORF3"
FT   /note= "unique long 47 (UL47)-like gene"

7158..7161
FT   /tag= n
FT   /note= "TATA signal for ORF4"
FT   6748..7080
FT   /tag= o
FT   /label= "ORF4"
FT   /label= "ORF4"
FT   complement (6774..7154)
FT   /tag= p
FT   /label= "ORF4(RC)"
FT   7158..7161
FT   /tag= q
FT   /note= "TATA signal for ORF5"
FT   7245..8123
FT   /tag= r
FT   /label= "ORF5"
FT   /note= "glycoprotein gC gene"
FT   7245..7322
FT   /tag= s
FT   7323..8120
FT   /tag= t
FT   8200..8205
FT   /tag= u
FT   /note= "polyA site for ORF5"
FT   8289..8294
FT   /tag= v
FT   /note= "polyA signal for ORF5"
FT   8333..11290
FT   /tag= w
FT   /label= "ORF6"
FT   /note= "glycoprotein g60 gene"
FT   9623..10363
FT   /tag= x
FT   /note= "repeat region consists of approx. 23
FT   repeats of 30-36 bp"
FT   complement (9584..10462)
FT   /tag= y
FT   /label= "ORF6(RC)"
FT   11091..11094
FT   /tag= z
FT   /note= "potential TATA signal for ORF7"
FT   11098..12402
FT   /tag= aa
FT   /label= "ORF7"
FT   12455..12448
FT   /tag= ab
FT   /note= "TATA signal for ORF8"
FT   12510..13598
FT   /tag= ac
FT   /label= "ORF8"
FT   /note= "glycoprotein gI gene"
FT   12510..12575
FT   /tag= ad
FT   12576..13595
FT   /tag= ae
FT   complement (13253..13786)
FT   /tag= af
FT   /label= "ORF8(RC)"
FT   13705..13708
FT   /tag= ag
FT   /note= "TATA signal for ORF9"
FT   13792..15291
FT   /tag= ah
FT   /label= "ORF9"
FT   /note= "glycoprotein gE gene"
FT   13792..13845
FT   /tag= ai
FT   13846..15288
FT   /tag= aj
FT   15116..15119
FT   /tag= ak
FT   /note= "TATA signal for ORF10"
FT   15298..16080
FT   /tag= al
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FT      /label= ORF10
FT      repeat_region
FT      16004..18912
FT      /tag= am
FT      16129..17013
FT      /tag= an
FT      CDS
FT      CDS
FT      complement (17380..18216)
FT      /tag= ao
XX      W09629396-A1.
XX      PD
XX      26-SEP-1996.
XX      PF
XX      21-MAR-1996; 96WO-US03916.
XX      PR
XX      06-JUN-1995; 95US-0468190.
XX      PR
XX      23-MAR-1995; 95US-0410121.
XX      (SYTR ) SYNTRO CORP.
XX      PA
XX      Cochran MD, Wild MA:
XX      PI
XX      MPI: 1996-443172/44.
XX      P-PDB: AAM06782, AAM06783, AAM06784, AAM06785, AAM06786, AAM06787,
DR      AAM06788, AAM06789, AAM06790, AAM06791, AAM06792, AAM06793, AAM01415,
DR      AAM01416.
XX      DR
XX      Recombinant infectious laryngotracheitis virus with deletion in the
PT      glycoprotein G, g1 or US2 gene, etc. - useful for vaccines against
PT      infectious laryngotracheitis in poultry
XX      PS
XX      Example 11; Page 138-154; 216pp: English.
XX      CC
XX      The nucleotide sequence of 19,912 bp of contiguous DNA (AAT44385)
CC      from the unique short and flanking region of infectious
CC      laryngotracheitis virus (ILTV) contains the entire 13,098 bp unique
CC      short region (see also AAT44384) and includes 17 open reading frames
CC      that encode proteins (AAM06782-94, AAM01415-16) of over 100 amino
CC      acids, 10 of which show homology to other virus genes. Novel
CC      recombinant, attenuated ILTV comprises the ILTV genome contg. a
CC      deletion in the unique short region, esp. in the glycoprotein gC,
CC      g1, US2, ORF4, UL47-like or g60 gene. The attenuated virus is
CC      useful as a vaccine against ILTV. A foreign gene encoding an
CC      antigen e.g. from another avian virus can be inserted into the US2,
CC      UL47-like, ORF4, gC, g60 or g1 gene to provide a multivalent
CC      vaccine for chickens and other poultry. Deletion of the gC or g1
CC      gene provides as a negative marker to distinguish vaccinated from
CC      infected animals.
XX      SO
XX      Sequence 18912 BP; 4416 A; 5261 C; 5251 G; 3984 T; 0 other:

alignment_scores:
    Quality: 2311.00      Length: 434
    Ratio: 5.325          Gaps: 0
    Percent similarity: 100.000    Percent identity: 100.000

alignment_block:
US-09-994-064-11 x AAT44385 ..

Align seg 1/1 to: AAT44385 from: 1 to: 18912

1 MethisATGPrOHISLeuAqRgHISserARgYTYrAlaLysGlyG1 17
|||||
11098 ATGCACCGCTCCATCTCAGAGCGCACTCGGTACTACGCGAAGAGAGA 11147

17 uValleuAnuLySHISmetASpCYGlyLyLysARgCYsSerGlyA 34
|||||
11148 GGTGCTTAACAACACATGATGGCGTGGAAACGGTGGCTCTAGGCG 11197

34 laAlaValPheThrLeuPheThrPThrCysValARgILleMetARgLuHIS 50
|||||
11198 CAGCTGTATCTACTCTTTCTTGACTGTGTGAGGATATATGCGGGAGCAT 11247

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51 lIleCYSPheValARgASnAlaMetASpARgHISLeuPheLeuARgASnAl 67
|||||
11248 ATCTGCTTTGTAGCGCAACGCTATGAGCCGCCATTATTTTGTAGGAATGC 11297

67 aPheTrPThrILleValLeuLeuSerSerPheAlaSerGlnSerThrAlaA 84
|||||
11298 TTTTGGACTATCGTACTGCTTTCTTCTTCTGCTGCGTACGACAGCCGCCG 11347

84 laValThrTYrASpTYrILleuGlyARgARgAlaLeuASpAlaLeuThr 100
|||||
11348 CCGTCACGTACGACTACATTTTATAGCGCGCTGCGCTGACGCTACAC 11397

101 lIleProAlaValGlyProTYrASnARgTYrLeuThrARgValSerARgG1 117
|||||
11398 ATACCGCGCGGCTTGCCCGCTATACAGATACCTCCTAGGATATCAAGAG 11447

117 yCYsASpValValGluLeuASnProILleSerASnValASpASpMetILes 134
|||||
11448 CTGCGACGCTGTGAGACTCAACCCGATTCTTAACGTGGACGACATGATAT 11497

134 eRAlaAlaLysGluLySGlyLyGlyProPheGluAlaSerValVal 150
|||||
11498 CGCGCGCAAGAAAGAAAGAGAGGGGCCCTTTGAGGCCCTCCGCTC 11547

151 TrpPheTYrValILleYsGlyASpASpGlyGluASpLYSTyrCYsProIL 167
|||||
11548 TGGTTCTACGTGATTTAAGGCGCACGCGCGAGGACCAATCTGTCAT 11597

167 eTYrARgLYSGlyTYrARgGluCYsGlyASpValGlnLeuLeuSerGlnC 184
|||||
11598 CTATACAAAAGATACAGGAATGTGGCAGCTACACTGCTATCTGANT 11647

184 ySAIAlaValGlnSerAlaGlnMetTrpAlaValASpTYrValProSerThr 200
|||||
11648 GCCCCTTCATATGACAGATGTGGCAGTGAGTATCTCTAGCAC 11697

201 LeuValSerARgASnGlyAlaGlyLeuThrILlePheSerProThrAlaI 217
|||||
11698 CTGTATTCGGGAATGGCGGGAGTACTATATTTCTCCCACTGCTC 11747

217 aLeuSerGlyGlnTYrLeuLeuThrLeuLysILleGlyARgPheAlaGlnT 234
|||||
11748 GCTCTGCGCATACTTGCTGTGACCTGAAATCGGAGATTTGGCCAA 11797

234 hRAlaLeuValThrLeuGluValASnASpARgCYsLeuLysILleGlySer 250
|||||
11798 CAGCTCTGTAACCTAGAAATTAAGATCGCTGTTAAAGATCGGGGTG 11847

251 GluLeuASnPheLeuProSerLYsCYSTrPThrThrGluGlnTYrGlnH 267
|||||
11848 CAGCTTAACCTTTTACCGTGAATGTGTGACAAACAGACATATCAGAC 11897

267 rGlyPheGlnGlyGluHISLeuTYrProILleAlaASpThrASnThrARgH 284
|||||
11898 TGGATTTCAAGCGCAACACCTTATCCGATCGACAGACCAATAATACAGAC 11947

284 lSAIlaASpASpValTYrARgLYSTyrGlyLysPILleuGlnARgTYrASn 300
|||||
11948 ACGCGAGACGATATATCGGGGATACGAAGATATTTGCGACCGCTGAAT 11997

301 ASnLeuLeuARgLYsLYsASnProSerAlaProASpProARgProASpSe 317
|||||
11998 AATTTGCTGAGAGAAAGAAATCCTAGCGCGCAGACCTCGTCAGATAG 12047

317 rValProGlnGluILleProAlaValThrLYsLYsAlaGluGlyARgThrP 334
|||||
12048 CGTCCCGCAAGAAATTCGCCGTATACCAAGAAAGCGGAGGGCGCACCC 12097

334 rASpARlaGluSerSerGlyLysLYsAlaProProGluASpSerGluASp 350
|||||
12098 CGGACGCGAAGAAAGCGCAAGAAAGAGGCCCTCCAGAGACTCGGAGAGAC 12147

351 ASpMetGlnAlaGluAlaSerGlyGluASnProAlaAlaLeuProGluAS 367

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12148 GACATGACGAGAGAGGCTTGTGAGAAATCTCGCCGCCCTCCCGAAGA 12197
367 PASGGLVALPProGLuSPHrGLuHISASPSPProASnSerASpProA 384
12198 CGACGAAAGTCCCGGAGACACCGGAGACAGATGATCAAACTCGATCCTG 12247
384 SPFTYrTASpMetProAlaValIleProValIleGluThrThrllys 400
12248 ACATATTCAATGACATCCCGCGGTGATCCCGGTGAGAGAGACTACTAA 12297
401 SerSerAsnAlaValSerMetProIlePheAlaIaPheValAlaCysAl 417
12298 AGTTCTATATGCCGCTCTCCATCCCATATTCGGCGCTTCGAGCTCGGC 12347
417 aValAlaIleValIleGluLeuValITrpSerIleValIleCysAlaArgS 434
12348 GGTGCGCTGCTGGGCTACTGTTGGAGCATGCTAAATGCGCGGTA 12397
434 er 434
12398 GC 12399
seq_name: /SID1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:AAQ22986
seq_documentation_block:
ID AAQ22986 standard; DNA; 3502 BP.
XX
XX AAQ22986;
AC
XX
XX 02-NOV-1992 (first entry)
DE
XX Sequence of ILTV gp60 gene.
XX
XX Subunit vaccine; immunogen; glycoprotein; promoter; ss.
XX
XX Infectious laryngotracheitis virus.
XX
XX Key Location/Qualifiers
XX TATA_signal 294..299
XX CDS 339..3326
XX repeat_unit 1692..1712
XX repeat_unit 1755..1775
XX repeat_unit 1824..1841
XX repeat_unit 1857..1871
XX repeat_unit 1923..1943
XX repeat_unit 1986..2006
XX repeat_unit 2019..2039
XX repeat_unit 2115..2129
XX repeat_unit 2211..2228
XX repeat_unit 2241..2261
XX repeat_unit 2304..2324
XX repeat_unit 2334..2351
XX
XX WO9203554-A.
XX
XX 05-MAR-1992.

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XX
PF 23-AUG-1991: 91MO-AU00383.
PR 24-AUG-1990: 90AU-0001937.
XX
PA (WEBS-) WEBSTER A PTY LTD.
XX
PI Sheppard MG, Prideaux C, Johnson M, Fahey KJ, York JJ;
PI Kongsuwan K;
XX
DR MPI: 1992-096898/12.
DR P-PsDB; AAR22234.
XX
PT Vaccines against ILTV for use in chickens - comprises
PT non-infectious sub-units or live recombinant viruses and may be
PT administered by aerosol
XX
PS Claim 14; Fig 6; 122pp; English.
XX
CC The inventors claim a non-infectious subunit vaccine for use against
CC ILTV which comprises a glycoprotein of ILTV. They also claim DNA
CC encoding the vaccine, a synthetic polypeptide displaying the
CC antigenicity of the 205k complex or 60k ILTV glycoprotein and a
CC recombinant ILTV with heterologous DNA inserted into a non-essential
CC region of the genome; and a recombinant DNA mol. comprising an ILTV
CC promoter region operatively linked to a heterologous DNA sequence.
CC The promoter region is the ILTV gp60 promoter, gp205 (9pb) promoter
CC or the ORF3 promoter region. KpnK/ORF3 is located 5' of the gp60
CC gene. The deduced AA sequence of the gp60 gene has 19 hydrophobic
CC AA residues at the N-terminus which may correspond to the signal
CC sequence. A second region of hydrophobic AAs (posn. 960 to 989) at
CC the C-terminus could function as a transmembrane anchor sequence.
CC There are nine potential N-linked glycosylation sites on the ILTV
CC gp60 protein. One of these sites at residue 677, may not be active
CC due to the presence of a proline residue within the N-X-S/T signal.
CC There are repeated sequences within the ILTV gp60 coding region.
CC They are not perfectly conserved but several copies had diverged so
CC that only 4 AAs out of 7 were conserved in all 13 copies of the
CC repeats. There is no significant homology between the protein and
CC any sequenced herpesvirus proteins in the database called PIR.
XX
SQ Sequence 3502 BP; 845 A; 969 C; 920 G; 768 T; 0 other:

alignment_scores:
Quality: 648.00 Length: 123
Ratio: 5.311 Gaps: 0
Percent Similarity: 99.187 Percent Identity: 96.748

alignment_block:
US-09-994-064-11 x AAQ22986 ..

Align seg 1/1 to: AAQ22986 from: 1 to: 3502

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|||||
3134 ATGCACGCTCCTCATCTTAGACGACCTCGCTTACTACGGAAGGAGA 3183
17 uValleuAsnLysHISMeLaspCysGlyGlyLysArgCysSerGlyA 34
|||||
3184 GGTGCTTAGACGACACATGATGCGGTGGGAAACGGTGCATCGACGGC 3233
34 laAlaValPheThrLeuPheTrpThrcysValArgIleMetArgGluHIS 50
|||||
3234 CACGTGATTCACCTTTTCGACTGTGTACAGATATTCGGGAGAGCAT 3283
51 IleCysPheValArgAsnAlaMetLaspArgHisLeuPheLeuArgAsnAl 67
|||||
3284 ATCTGCTTTGTAGCGAACGCTATGACCGCCCATTTATTTTGAAGAAATC 3333
67 aPheTrpThrIleValleuLeuSerSerPheAlaSerGlnSerThrAlaA 84
|||||
3334 TTTTGGACTATGCTACTGCTTCTCTCTGCTTACGACGACGACGCGC 3383

```

84 laValThrTyrAspTyrIleLeuGlyArgAlaLeuAspAlaLeuThr 100  
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 3384 CCGTACAGCAGTACATTTAGCCGCGCTCGACGCGCTAACCC 3433  
 101 IleProAlaValGlyProTyrAsnArgTyrLeuThrArgValSerArg1 117  
 |||  
 3434 ATACCGCGCGTGGCCGCTATACAGATACCTACTAGGCTATCAGAGG 3483  
 117 yCysAspValValGluLeu 123  
 |||  
 3484 CTGCGAGCTGTGCGAGCTC 3502  
 seq\_name: /SIBS1/gcdata/geneseq/geneseqn-emb1/NA1989.DAT.AAN90524  
 seq\_documentation\_block:  
 ID AAN90524 standard; DNA; 1602 BP.  
 XX AAN90524;  
 AC  
 DT 16-NOV-1989 (first entry)  
 XX  
 DE Herpes Simplex virus-1 gd gene and flanking regions.  
 XX  
 KW Herpes Simplex virus-1; gd gene; diagnostic test kit;  
 KM membrane-free polypeptide; antibody; anti-antibody; detection.  
 XX  
 OS Herpes simplex virus-1.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 237..1415  
 FT /\*tag= a  
 XX  
 A08930061-A.  
 PN  
 PD 22-JUN-1989.  
 XX  
 PF 17-FEB-1989; 89AU-0030061.  
 XX  
 PR 30-AUG-1983; 83AU-0030061.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Berman PW, Lasky LA;  
 XX  
 DR WPT: 1989-234099/33.  
 DR P-PSDB: AAP90165.  
 XX  
 PT Diagnostic test kit - contains molecularly cloned, truncated  
 CC membrane-free deriv. of polypeptide and complementary antibody  
 CC or anti-antibody.  
 CC  
 PS Disclosure: fig 1; 88pp; English.  
 XX  
 CC Herpes Simplex virus-1 gd gene (see corresp. AAP90887) and flanking  
 CC regions. This was used to make truncated membrane-free derive.  
 CC with antigenic determinants capable of specifically binding  
 CC complementary antibody (Ab). The patent claims  
 CC a diagnostic kit contg. the deriv. and the Ab or anti-Ab,  
 CC for detecting HSV infection. See AAN90523-6, AAN90529-30, AAP90165,  
 CC and AAP90166.  
 XX  
 SQ Sequence 1602 BP; 310 A; 543 C; 462 G; 287 T; 0 other;

alignment\_scores:  
 Quality: 200.00 Length: 489  
 Ratio: 0.943 Gaps: 21  
 Percent Similarity: 43.354 Percent Identity: 22.086

alignment\_block:  
 US-09-994-064-11 x AAN90524 ..

Align seg 1/1 to: AAN90524 from: 1 to: 1602  
 2 HisArgProHisLeuArgArgHisSerArgTyrTyrAlaLeuGlyLeu 18  
 :|||  
 54 TACGACACACAGCAGAACCC.....CCTAAGGGAGAGG 88  
 18 IleuAsnLysHisMetAspCysGlyLysArgCysCysSerGlyAla 35  
 :|||  
 89 GCCATTTTACGAGGAGGAGGGGTATACAAAGCTGTCTTAAAAAGCAG 138  
 35 laValPheThrLeuPheThrPheThrCysValArgIleMetArgLys 50  
 :|||  
 139 GGGTATAGGAGTGTTCGGTCAT.....AACCTTACGCGGAGACCA 182  
 51 .....IleCysPheValArgAs 56  
 :|||  
 183 ACTACCCCGATCATGATTCCTTAAAGTCTCTTTGTGTGTCGTTTC 232  
 56 naIaMetAspArgHisLeuPheLeuArgAsnaIaPheThrIleValL 73  
 :|||  
 233 CGGTATG..... 239  
 73 euleuSerSerPheAlaSerGlnSerThrAlaAlaValThrTyrAsp 89  
 :|||  
 240 .....GGGGGGCTGCCAGAGTTGGGGCGGTGATTTGTTGTCTC 284  
 90 IleLeuGlyArgArg..... 94  
 :|||  
 285 ATAGTGGGCTTCATGGGTCGCCGCAATATGCTTGGCGATGCTTC 334  
 95 .....AlaL 96  
 :|||  
 335 TCTCAAGATGCCGACCCCATGCTTTCGCGGCAAAAGACTTCGGTTT 384  
 96 euaSpsAlaLeuThrIlePro.....Ala 103  
 :|||  
 385 TGGACCCAGCTGACGACCTCCGGGGGTCCGGCGGTATACACATCCAG 434  
 104 ValGlyProTyrAsnArgTyr.....Le 111  
 :|||  
 435 GCGGGCTTACCGAACCCGTTCCAGCCCCCAGCCTCCGATCAGGTTTA 484  
 111 uThrArgValSerArgGlyCysAspValValGluLeuAsnProIleSer 128  
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 485 CCGCGCTGTGAGCGCGCTGCGCAGCGTCTCTTAAAGCAGCAGCTCG 534  
 128 snValAspAspMetIleSerAlaAlaLysGluLysGluLysGlyPro 144  
 :|||  
 535 AGGCCCCCAGATTGTCGGGGGCTCCGAGAGAGCTCCGGAACAACACC 584  
 145 PheGluAlaSerValValTrrPheTyrValIleLysGlyAspAspGly 161  
 :|||  
 585 TACAACCTGACCATCGCTTGTTCGATG.....GAGG 619  
 161 uaSpsLysTyrCysProIleTyrArgLysGluTyrArgGlyCysGlyAsp 178  
 :|||  
 620 CAACGTGCTATCCCATCGCTCATGAGTACACCGAATGCTCTTACA 669  
 178 alGlnLeuLeuSerGluCysAlaValGlnSerAlaGlnMetTrpAlaVal 194  
 :|||  
 670 ACAAGTCTGTGGGGCTGTCCATCCGAAAGCAGACCCCGCTGG..... 713  
 195 AspTyrValProSer...ThrLeuValSerArgAsnGlyAlaGlyLeu 210  
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 714 AACTACATATGACAGCTTACGCGCGCTCAGGAGATATACCTGGGTCC 763  
 210 rIlePheSerProThrAlaAlaLeuSerGlyGlnTyrLeuLeuThrLeu 227  
 :|||  
 764 GATGCAAGCCCCCGCTTGAAGACCGCGGACGTGCTGCTGCTGTA 813  
 227 ysiIleGlyArgPheAlaGlnThrAlaLeuValThrLeuGlu.....Val 241  
 :|||  
 814 AGATTAACGACTGGACGAGATTAACACATTTATCCTGGAGACACCGAGCC 863







alignment\_scores:

Quality:	193.50	Length:	498
Ratio:	0.908	Gaps:	21
Percent Similarity:	42.771	Percent Identity:	21.486

Alignment block:  
US-09-994-064-11 x AAN40070 ..

Align seg 1/1 to: AAN40070 from: 1 to: 1608

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2  HisArgProHisLeuArgArgHisSerArgTyrTyrAlaLysGlyGluVal 18
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58  TACGACACACACGACGAAAC.....CCTAAGGGGAGAGG 92
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18  LleuAsnLysHisMetAspCysGlyGlyArgCysCysSerGlyAla 35
   ::::::::::::::::::::|
93  GCCATTTTACAGAGGAGGAGGATACAAAGTCTCTTAAAAAGCAG 142
   ::::::::::::::::::::|
35  LaValPheThrLeuPheThrCysValArgIleMetArgLHis... 50
   ::::::::::::::::::::|
143  GGGTTAGGAGTTGTTGGTCAT.....AGCTTCAGCGCAACGACCA 186
   ::::::::::::::::::::|
51  .....IleCysPheValArgAs 56
187  ACTACCCGATCATCAGTTATCTTAAGGTCTCTTGTGTGTGCTTC 236
   ::::::::::::::::::::|
56  nAlaMetAspArgHisLeuPheLeuArgAsnAlaPheTrpThrIleVal 73
   ::::::::::::::::::::|
237  CGGTATG..... 243
73  euleuSerPheAlaSerGlnSerThrAlaAlaValThrTyrAspTyr 89
   ::::::::::::::::::::|
244  ....GGGGGAGTCGCCGAGTTGGGGGCGGTGATTTGTGTGCTC 288
90  IleuGlyArgArg..... 94
289  ATAGTGGCCCTCCATGGGGTCGGGGCAATATGCTTGGCGATGCCTC 338
95  .....AlaI 96
339  TCTCAGATGGCCGACCCCAATGCTTTCGGCGCAAAACCTTCGGGTCC 388
96  euAspAlaLeuThrIlePro.....Ala 103
389  TGGACACAGTACCGACCTCCGGGGTCGGCGGTATCCACATCCAG 438
104  ValGly.....ProTyrAsnArgTyr 110
439  GCGGGCTACCGGACCGTCCAGCCCCCAGCCCTCCGATCAGGGTTA 488
110  rLeuThrArgValSerArgGlyCysAspValValGluLeuAsnProIles 127
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489  CTACGCGGTGTGGAGCGCGCTCCGCAAGCTCTCTAAACACACCGCT 538
127  eAsnValAspAspMetIleSerAlaLysGluLysGluLysGlyLys 143
   ::::::::::::::::::::|
539  CCGAGGCCCCCAGATTGTCCGGGGCTCCGAAAGACGTCGGGAAACAA 588
144  PropheGluAlaSerValValTrpPheTyrValIleLysGlyAspAspG 160
   ::::::::::::::::::::|
589  CCTTACAAACGACCATCGCTGTGTTGCGATG.....GG 623
160  yGluAspLysTyrCysProIleTyrArgLysGluTyrArgLysGly 177
   ::::::::::::::::::::|
624  AGGCAACTGTGCTATCCCATCAGGTATGAGTACACGAAATGCTCT 673
177  spValGlnLeuLeuSerGlyAlaValGlnSerAlaGlnMetTrpAla 193
   ::::::::::::::::::::|
674  ACAACAAGTCTCTGGGGCTGTCCATCCGACGACGACCCGCTGG... 720
194  ValAspTyrValProSer...ThrLeuValSerArgAsnGlyAlaGly 209
   ::::::::::::::::::::|
721  ...AACTACTATGACAGCTTCAGCGCGCTCAGCAGATATACCTGGGTT 767

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209  uThrIlePheSerProThrAlaAlaLeuSerGlyGlnTyrLeuLeuThr 226
   ::::::::::::::::::::|
768  CCTGATGACAGCCCCCGGCTTGGACCGCGCGACGTGCTGGGGCTCG 817
226  eulysIleGlyArgPheAlaGlnThrAlaLeuValThrLeuGlu..... 240
   ::::::::::::::::::::|
818  TGAAGATTAACGACTGGACGAGATTACACAGTTTATCTGGAGACCGCA 867
241  ValAsnAspArgCysLeuLysIleGlySerGlnLeuAsnPheLeuProSe 257
   ::::::::::::::::::::|
868  GCCAAGGGCTCGTGT...AAGTACGCTCCCGCTGCGCATCCCGCGCTC 914
257  rLysCysTrpThrThrGluGlnTyrGlnThrGly..... 268
   ::::::::::::::::::::|
915  AGCCTGCTCTCCCGCAGGCTTACACAGAGGGGTGAGGTGACAGCA 964
269  .....PheGlnGlyGlnHisLeuTyrProIleAlaAsp 279
965  TCGGATGCTGCCCCGCTTCATCCCGGAAACACAGCAGCCTGCGCTTA 1014
280  ThrAsnThrArgHisAlaAspAspValTyrArgLysGluAspIleLe 296
   ::::::::::::::::::::|
1015  TACAGCTTGAAGATCGCCGG..... 1035
296  uGlnArgTrpAsnAsnLeuLeuArgLysLysAsnProSerAlaProAsp 313
   ::::::::::::::::::::|
1036  ....TGGCAC.....GGGCGCAAGGCCCA...T 1057
313  rArgProAspSerValProGlnGluIleProAlaValThrLysLysAla 329
1058  ACAGAGACACCTGCTGCCCGGACGCTG..... 1086
330  GluGlyArgThrProAspAlaGlnSerGlyLysAlaProProG 346
   ::::::::::::::::::::|
1087  ...TCCGAGACCCCAACGCC.....ACGACGCAAGTACGCGCCGGA 1127
346  uAspSerGluAspAsp...MetGlnAlaGluAlaSerGlyLysAsnPro 362
   ::::::::::::::::::::|
1128  AGACCCGAGGATTCGCGCTTGGAGAGCCCGCTGGGAGCGGTGGCGC 1177
362  LaAlaLeuProGluAspAspGluValProGluAspThrGlnHisAspAsp 378
   ::::::::::::::::::::|
1178  CGCAATTCACCAACATCGCACATCCGTCGATCCAGAGCCCGCGACG 1227
379  ProAsnSerAspProAspTyrTyrAsnAspMetProAlaValIlePro 395
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1228  CTTTACATCCCGCGGACCCCGCAACAAATGGGCTGATC..... 1269
395  IGluGlnThrThrLysSerSerAsnAlaValSerMetProIlePheAla 412
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1270  ....GCCGGCGCGTGGGGCGGAGTGTCTCTGGGAG 1300
412  lApheValAlaCysAlaValAlaLeuValGlyLeuLeuValTrp 426
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seq\_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT: AAN60545

seq\_documentation\_block:

ID AAN60545 standard; DNA: 1608 BP.

AC AAN60545:

02-JUL-1991 (first entry)

DE Sequence of a portion of the Herpes Simplex Virus type I (HSV-I)

DE glycoprotein D (gD) gene.

XX Probe: hybridisation; ds.

XX Herpes simplex virus type I.

XX

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FH Key Location/Qualifiers
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WO607387-A.
PD 18-DEC-1986.
PF 13-JUN-1986; 86WO-0001280.
XX
PR 13-JUN-1985; 85US-0744800.
XX
XX (AMGE-) AMGEN.
PA (ABBO ) ABBOTT LABORATORIES.
PA (NOVO ) NOVO IND A/S.
PI Snilman DL, Stroupe SD.
XX WPI: 1986-346610/52.
DR Nucleic acid hybridisation assays - suitable for assaying
XX double-stranded DNA
XX
PS Example; Table I, Pages 15-19; 47pp; English.
XX
CC The examples illustrate the practice of the method of the invention.
CC Specifically demonstrated are hybridisation assays employing the two-
CC probe system to detect and quantitate the amount of desired target
CC sequence in a solution. Portions of the plus and minus strands of
CC HSV-I gd gene were used as probes.
XX
SQ Sequence 1608 BP; 313 A; 541 C; 466 G; 288 T; 0 other;

alignment_scores:
Quality: 193.50 Length: 498
Ratio: 0.908 Gaps: 21
Percent Similarity: 42.771 Percent Identity: 21.486

alignment_block:
US-09-994-064-11 x AAN60545 ..

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18 IleuAsnLysHisMetAspCysGlyGlyLysArgCysCysSerClyAla 35
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93 GCCATTTTACGAGGAGGAGGGGTATACAAAGTCTTTAAAGAAGCAG 142
35 laValPheThrLeuPheThrThrCysValArgIleMetArgGluHis... 50
:::|||||
143 GGGTTAGGAGGTGTCTCGGTCAAT.....AAGCTTACGGCGAAGACCA 186
51 .....IleCysPheValArgAs 56

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56 nAlaMetAspArgHisLeuPheLeuArgAsnAlaPheTrpThrIleVal 73
237 CGGTATG..... 243
73 euleSerSerPheAlaSerGlnSerThrAlaIleValThrTyraSpyr 89
244 .....GGGGGACTGCGCCGAGTTGGGGCGGTATTTGTTGTGTC 288
90 IleuGlyArgArg..... 94
289 ATAGTGGCCCTCCATGGGGTCGGGCAATATGCTTGGCGATGCTC 338
95 .....AlaL 96
339 TCTCAAGATGCGCCGACCCCAATCGCTTTCGGCGCAAGACCTTCGGTCC 388
96 euAspAlaLeuThrIlePro.....Ala 103
389 TGGACCCAGCTACGACCCCTCCGGGGTCCGGCGGTACCATTCAG 438
104 ValGly.....ProTyraArgTy 110
439 GCGGGCCCTACCGGACCCGTTCCAGCCGCCAGCCCTCCGATCAGCGTTTA 488
110 rLeuThrArgValSerArgIlyCysAspValValGluLeuAsnProIles 127
489 CTACGCCCTGTGTGGAGCGCGCTCCGCGAGGTCTCTTAAGCAGACCGT 538
127 eAsnValAspAspMetIleSerAlaAlaIlyGluIlyGluSly 143
539 CGGAGGCCGCCAGATTGTCGGGGGCTCCGAGACGTCCGGAACAA 588
144 ProPheGluAlaSerValValTrpPheTyraIleIlySlyAspAspG 160
589 CCTACACACCTGACCATGCTGTGGTGGATG.....GG 623
160 yGluAspIlyTyrcysProIleTyraArgIlyGluTyraArgIlyGlu 177
624 AGGCAAGTGTCTATCCCATCAGGTGATGAGTACACCATGCTCTCT 673
177 spValGlnLeuLeuSerGluCysAlaValGlnSerAlaGlnMetTrpAla 193
674 ACAACAATCTCTGGGGCTGTCCCATCCAGACGACGCCGCCGCG... 720
194 ValAspTyraValProSer...ThrLeuValSerArgAsnGlyAlaGlyLe 209
721 ...AACTACTATGACAGCTTCAAGCCCTCAGCGAGATACCTGGGGTT 767
209 uThrIlePheSerProThrAlaAlaLeuSerGlyGlnTyraLeuLeuThr 226
768 CCTGTGACGCGCCCGCGTTGAGACCGCGGACGATGCTGGCGCG 817
226 euIlyIleGlyArgPheAlaGlnThrAlaLeuValThrLeuGlu..... 240
818 TGAAGATTAACGACTGAGACGAGATTACACAGTTATCTGAGACACGA 867
241 ValAsnAspArgCysLeuIlyIleGlySerGlnLeuAsnPheLeuProSe 257
868 GCCAAGGGCTCTGT...AAGTACGCGCTCCCGCGCATCCCGCGCTC 914
257 rIlyCysTrpThrThrGluGlnTyraGlnThrGly..... 268
915 AGCTGCGCTCTCCCGCGCGCTTACACGACGAGGGGTGACGGTGACACA 964
269 .....PheGlnGlyGlnHisLeuTyraProIleAlaAsp 279
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1058 ACACGACGACCCCTGCTGCCCGGAGCTG..... 1086
330 GluGlyArgTrpProAspAlaGluSerGluIlySlyAlaProProG 346
1087 ...TCCGAGACCCCAAGCC....ACGAGCCAGAACTCGCCCGCA 1127
346 uAspSerGluAspAsp...MetGlnAlaGluAlaSerGlyGluAsnPro 362
1128 AGACCCCGAGATTCGGCCCTTGGAGAGACCCCGGGGAGCGTGGCC 1177
362 lAlaLeuProGluAspAspGluValProGluAspThrGluHisAsp 378
1178 CGCAATCCCAACCAACTGGCAGATCCGTCATGAGAGACCCCGCAGC 1227
379 ProAsnSerAspProAspTyraSyrAsnAspMetProAlaValIlePro 395
1228 CCTTACCATCCCGCGCGCACCCCGAACAACATGGCGCTGATC..... 1269
395 lGluGluThrThrIlySerSerAsnAlaValSerMetProIlePheAla 412
1270 .....GCCGGCGCGTGGCGCGCAGTCTCCGCGCAG 1300
412 lApeValAlaCysAlaValAlaLeuValGlyLeuLeuValTrp 426
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ID AAZ10959 standard; DNA; 1185 BP.
AC AAZ10959;
XX
AC AAZ10959;
XX
DT 29-OCT-1999 (first entry)
XX
DE HSV-1 glycoprotein D coding sequence.
XX
KW glycoprotein D; gpD; recombinant antigen library; disease-related antigen;
KW multi-valent antigenic polypeptide production; infection; allergen;
KW asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy;
KW multiple sclerosis; inflammatory condition; cancer; contraception;
KW immune response; ss.
XX
OS Herpes simplex virus.
XX
PN W09941383-A1.
XX
PD 19-AUG-1999.
XX
PF 10-FEB-1999; 99MO-US02944.
XX
PR 23-OCT-1998; 98US-0105509.
PR 11-FEB-1998; 98US-0021769.
PR 11-FEB-1998; 98US-0074294.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Bass SH, Howard R, Punnonen J, Stemmer WPC, Whalen RG;
XX
DR WPI; 1999-518452/43.
XX
PT Recombinant multi-valent antigenic polypeptide produced by
PT recombinant nucleic acid sequences and screening, used in vaccines
PT against e.g. infections and cancer
XX

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[illegible]



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; Sequence 19, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1305
; US-08-477-459-19

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Ratio: 5.325 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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701 CACCTCTCGTAACCTAGAGTTAACGATCGCTTTAAAGATCGGGTGC 750
251 GlnLeuAsnPheLeuProSerLysCysTrpThrThrGlnGlnTyrGln 267
751 CAGCTTAACCTTTTACCGTGAATGCTGGACAACAGAAAGATATCAGAC 800
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317 rValProGlnGlyIleProAlaValThrLysLysAlaGlyGlyArgThr 334
951 CGTCCCGCAAGAAATTCCTGCTGTAACCAAGAAAGCGAAGGGCGACCC 1000
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; Sequence 19, Application US/08479869
; Patent No. 6123949
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D. Mark D
; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 .and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,869
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/024,156
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
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: TELEPHONE: (212)977-9550  
 : TELEFAX: (212)664-0525  
 : TELEX: 422523  
 : INFORMATION FOR SRO. ID NO: 19:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1305 base pairs  
 : type: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)  
 : HYPOTHEICAL: NO  
 : ANTI-SENSE: NO  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 1..1305  
 : US-08-479-869-19

alignment\_scores:  
 Quality: 2311.00 Length: 434  
 Ratio: 5.325 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-994-064-11 x US-08-479-869-19 ..

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 17 UValLeuAsnLysHisMetAspCysGlyLysArgCysCysSerGlyA 34  
 51 GGTGCTTAACAAACATGATTCGGTGGAAACGTCCTGCTCGAGGG 100  
 34 LaAlaValPheThrLeuPheThrCysValArgLleMetArgLysHis 50  
 101 CACCTGATTCACCTCTTTCTGACCTTGCTGAGATTAATGCGGAGAT 150  
 51 IleCysPheValArgAsnAlaMetAspArgHisLeuPheLeuArgAsn 67  
 151 ATCTGCTTTGACGCAACCTATGACCGCCCATTTATTTTGAGGATGC 200  
 67 aPheTPTThrIleValLeuLeuSerSerPheAlaSerGlnSerThrAla 84  
 201 TTTTGGACTATCGTACTCTTCTTCTTCTGCTAGCCAGACCGCCG 250  
 84 LaValThrTyrAspTyrIleLeuGlyArgArgAlaLeuAspAlaLeuThr 100  
 251 CCGTCACGTACGACTACATTATTAGGCGCGCGCTCGACCGCTAAC 300  
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 : Sequence 19 Application US/08486414B  
 : Patent No. 6136318  
 : GENERAL INFORMATION:  
 : APPLICANT: Cochran, Mark D.  
 : APPLICANT: Junker, David E.  
 : TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF  
 : FILE REFERENCE: 42771D

;; CURRENT APPLICATION NUMBER: US/08/486,414B  
;; CURRENT FILING DATE: 1995-06-07  
;; NUMBER OF SEQ. ID NOS: 46  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 19  
;; LENGTH: 1305  
;; TYPE: DNA  
;; ORGANISM: Fowlpox virus  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(432)  
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;; GENERAL INFORMATION:  
;; APPLICANT: Syntro Corporation, et al.  
;; TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof  
;; NUMBER OF SEQUENCES: 20  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: John P. White  
;; STREET: 30 Rockefeller Plaza  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA

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; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01826A
; FILING DATE: 28-FEB-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
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; LOCATION: 1..1305
; PCT-US94-01826A-19

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; APPLICANT: Syntho Corporation, et al.  
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
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; APPLICATION NUMBER: PCT/US94/02252A  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White Esq, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1305 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
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; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patent Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03916
; FILING DATE: 23-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/126,597
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:

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; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39116-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
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 ; Sequence 59, Application PC/TUS9603916  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wild, Martha A.  
 ; APPLICANT: Cochran, Mark D.  
 ; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patentln Release #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/03916  
 ; FILING DATE: 23-MAR-1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/126,597  
 ; FILING DATE: 24-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 39116-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 59:  
 ; SEQUENCE CHARACTERISTICS:  
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 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
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? Patent No. 5654174
? GENERAL INFORMATION:
? APPLICANT: Cohen, Gary H.
? APPLICANT: Eisenberg, Roselyn J.
? APPLICANT: Nicola, Anthony
? TITLE OF INVENTION: Herpes Simplex Virus Glycoprotein D
? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? STREET: 6300 Sears Tower, 233 S. Wacker Drive
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/499,568
? FILING DATE:
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: No. 5654174and, Greta E.
? REGISTRATION NUMBER: 35,302
? REFERENCE/DOCKET NUMBER: 32813
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 474-6300
? TELEFAX: (312) 474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1608 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
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; Sequence 1, Application US/07829947A
; Patent No. 5679348
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; GENERAL INFORMATION:
; APPLICANT: NESBURN, ANTHONY B
; APPLICANT: WECHSLER, STEVEN L
; APPLICANT: GHIST, HOMAYON
; TITLE OF INVENTION: IMMUNOTHERAPY FOR RECURRENT HSV
; NUMBER OF INVENTIONS: 1
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 WEST 6TH ST.
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/829,947A
; FILING DATE: 19920203
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAAKE, DEBORAH L
; REGISTRATION NUMBER: 34,832
; REFERENCE/DOCKET NUMBER: 194/284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1204 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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221 nTyrlleuLeuThrleuLysIleGlyArgPheAlaGlnThrAlaLeuVal 238
585 GTACTCGGCTCGTAGAATAAAGACTGACGAGATTAACAGCTTTA 634
238 hrleuGlu.....ValAsnAspArgCysLeuLysIleGlySerGlnLeu 252
635 TCCGTGGAGACCGAGCCAGGGCTCTGT...AAGTACGCGCTCCGCTG 681
253 AsnPheLeuProSerLysCysTrpTrpThrGluGlnTyrglnThrGly.. 268
682 CGCATCCCGCGTCAAGCTGCTCTCCCGACGCTACACGAGGAGGT 731
269 .....PheGlnGlyGlnHisLeu 275
732 GACGCTGACAGCATCGGATGCTGCCCGCTTCATCCCGAGAACAGC 781
275 yrProIleAlaAspThrAsnThrArgHisAlaAspAspValTyArgGly 291
782 GCACCGCTCGCGTATACAGCTTGAGATCGCGG..... 816
292 TyrlGluaspIleLeuGlnArgTrpAsnAsnLeuLeuArgLysAsnPr 308
817 .....TGCGAC.....GGGCG 827
308 oSerAlaProAspProArgProAspSerValProGlnGluIleProAlaV 325
828 CAAGGCCCCA...TACAGAGCAACCTGCTGCCCGCGAGCTG..... 867
325 alThrLysLysAlaGluGlyArgThrProAspAlaGluSerSerGluLys 341
868 .....TCCGAGACCCCCAACGCC.....ACGCACCA 894
342 LysAlaProProGluaspSerGluaspAsp...MetGlnAlaGluAla 357
895 GAACCTGCCCGGAGAGACCCGAGGATTTGGCCCTTGAGAGACCCGCT 944
357 rGlyGluAsnProAlaAlaLeuProGluaspAspGluValProGluAsp 374
945 GGGGACGCTGGCGCCGAATCCCACTGACATACCGTCGATCC 994
374 hrGluHisAspAspProAsnSerAspProAspTyTrpAsnAspMetPro 390
995 AGGAGCGCGGAGCGCTTACCATCCCGGCGACCCGGAACAACATGGC 1044
391 AlavalIleProValGluGluThrThrLysSerSerAsnAlaValSerme 407
1045 CTGATC.....GCCGCGCGGTGGCGG 1067

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407 tProIlePheAlaIlePheValAlaCysAlaValAlaLeuValGlyLeu 424
1068 CAGTCTCTGCGACCGCTGTATTTGC.....CGAATG 1102
424 euValTrp 426
1103 TGTACTGG 1110

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seq_documentation_block:
; Sequence 1, Application PC/TUS9300945
; GENERAL INFORMATION:
; APPLICANT: MESBURN, ANTHONY B
; APPLICANT: WECHSLER, STEVEN L
; APPLICANT: GHIAZI, HOMAYON
; TITLE OF INVENTION: IMMUNOTHERAPY FOR RECURRENT HSV
; TITLE OF INVENTION: INFECTIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 WEST 6TH ST.
; CITY: LOS ANGELES
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00945
; FILING DATE: 19930203
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/829,947
; FILING DATE: 03 FEB 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAAKE, DEBORAH L
; REGISTRATION NUMBER: 34,832
; REFERENCE/DOCKET NUMBER: 194/284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1204 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-00945-1

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Ratio: 1.180 Gaps: 14
Percent Similarity: 47.917 Percent Identity: 23.214

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306 CCTAAACGACCGTCGGAGGCCGCCAGATGTCCGGGGCTCCGAG 355
139 ysglulysgllygylprophgluAlaserValTrpPheTyrlle 155
356 ACGTCGGGAACACCTTACAACTGACCATCGCTGTGGATG... 402
156 lysgllyAspasp1yglulasp1tyrCysProIleTyrlleTyrllygl 172
403 .....GGAGCAACTGTGTATTCCTCCATCAGCGTCATGAGTA 440
172 rArglucysgllyAspvalGlnleuSerIucysAlaValGlnSera 189
441 CACCAATCTCTTACACAAAGTCTGGGGCTTCCATCCGAAACC 490
189 laglmetrpAlaValaspTyrlleProSer...ThrlleuValsera 204
491 AGCCCGCTGG.....AACTACTATGACAGCTTCAGCCCGTCACGAG 534
205 AsnglyAlaGlyLeuThrIlePheSerProThrAlaIleuSerIyl 221
535 GATTAACCTGGGGTCTCTGATGACAGCCCGCTTGGAGCCGCGGAC 584
221 nTyrlleuLeuThrIleuLysIleGlyArpPheAlaGlnThrAlaVal 238
585 GTACCTGCGCTCTGTAAGATTAACGAGTGAAGATTACACAGTTTA 634
238 hrleuGlu.....ValasnAspArgCysleuLysIleGlySerGlnleu 252
635 TCCTGGAGACCGAGCCAAAGGCTCTGT...AAGTACGCTCCCGCTG 661
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269 .....PheGlnIleGlnIleuThr 275
732 GAGCGTGAACAGCATGGAGTCTGCGCCGCTTATCCCGAGAACACAG 781
275 yrProIleAlaAspThrAsnThrArgHisAlaAspValTyrlleGly 291
782 GCACCTCCCGCTATACAGCTTAAGATCCCGGG..... 816
292 TyrlGluAspIleLeuGlnArgTrpAsnAsnleuLeuLysLysAsnPr 308
817 .....TGGCAC.....GGGCC 827
308 oSerAlaProAspProArgProAspSerValProGlnIleProAlaVal 325
828 CAAGGCCCA...TACACGAGACCTGCTGCGCCCGGAGCTG..... 867
325 alThrIysLysAlaGlnIleArgThrProAspAlaGlnSerSerGluLys 341
868 .....TCCGAGACCCCGCAAGCC.....ACGCAACCA 894
342 LysAlaProProGluAspSerIleuAspAsp...MetGlnAlaGlnAla 357
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357 rGlyGluAsnProAlaIleuProGluAspAspGlnValProGluAsp 374
945 GGGGAGCGTGGCGCCCAATCCCAACAGTCACTACGCTGATGCC 994
374 hrGlnIleAspAspProAsnSerAspProAspTyrlleAsnAspMetPro 390
995 AGAGACCGCGAGAGCTTACATCCCGCGCACCCCGAACAACATGGCG 1044
391 AlaValIleProValGlnIleuThrIleLysSerSerAsnAlaValSerMe 407
1045 CTGATC.....GCGGCGCGGTGGCGG 1067
407 trProIlePheAlaIlePheValAlaCysAlaValAlaValGlyLeu 424
1068 CAGTCTCTGGCAGCCCTGGTCAATTGC.....GGAATTG 1102

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424 euValTrp 426
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seq_documentation_block:
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO; KAISHO, YOSHIIKO; YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO: 9:
; LENGTH: 1459
5182195-9

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Ratio: 1.173 Gaps: 14
Percent Similarity: 49.390 Percent Identity: 23.780

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345 CGCATCAGGTTTACTACACCGCTGTGGAGCGCGCTCCGAGCTGCT 394
122 uLeuAsnProIleSerAsnValAlaAspMetIleSerAlaIleValGln 139
395 CCTAAACGACCGCTGGAGGCCCGCCAGATTGTCCGGGGCTCCGAGAG 444
139 ysglulysgllygylprophgluAlaserValTrpPheTyrlle 155
445 ACGTCGGGAACACCTTACAACTGACCATCGCTGTGGATG... 491
156 lysgllyAspasp1yglulasp1tyrCysProIleTyrlleTyrllygl 172
492 .....GGAGCAACTGTGTATTCCTCCATCAGCGTCATGAGATA 529
172 rArglucysgllyAspvalGlnleuSerIucysAlaValGlnSera 189
530 CACCGAATGCTCTTACACAAAGTCTGGGGGCTGTCCCATCCGAAACG 579
189 laglmetrpAlaValaspTyrlleProSer...ThrlleuValsera 204
580 AGCCCGCTGG.....AACTACTATGACAGCTTCAGCGCGTCACGAG 623
205 AsnglyAlaGlyLeuThrIlePheSerProThrAlaIleuSerIyl 221
624 GATTAACCTGGGTCTCTGATGACAGCCCGCTTGGAGACCCCGCGG 673
221 nTyrlleuLeuThrIleuLysIleGlyArpPheAlaGlnThrAlaVal 238
674 GTACCTGCGGCTCTGTAAGATTAACGAGTGAAGGAGATTACACAGTTTA 723
238 hrleuGlu.....ValasnAspArgCysleuLysIleGlySerGlnleu 252
724 TCCTGGAGACCGAGCAAGGCTCTGT...AAGTACGCTCCCGCTG 770
253 AsnPhelLeuProSerIucysTrpThrIleGlnIleuThrIleGly 269
771 CGCATCCCGCGTACAGCTGCTCTCCCGCCAGCCTACACAGAGGGGT 820
269 eGlnIleGlnIleuThrProIle.....AlaAspThrAsnThr 283
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821 GACGGTGCACAGCTCGGATGTCGCCCGCTTCATCCCGAGAACCCAG 870
283 rGHISAlAspAspValTYrArgLYTYrGLuSpLLeuGLnATrP 299
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871 GC.....ACCGTCGCCGTATACAGCTTGAGATCGCGCGGTG 908
300 AAsnAnLeuAlaArgLYsAsnProSerAlaProAspProArProAs 316
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909 CAC.....GGGCCAAGGCCCA...TACACGACAC 937
316 pSerValProGLnGLuLeuProAlaValThrLYsLysAlaGLuLYrGT 333
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938 CCGTGGCCCGCTGAGCTG.....TCGACA 963
333 hProAspAlaGLuSerSerGLuLYsAlaProProGLuAspSerGLu 349
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964 CCCCACACGCC.....ACGACGCCAGAACCTGCCCGGAGAACCCCGAG 1007
350 AspAsp...MetGLnAlaGLuAlaSerGLuAsnProAlaAlaLeuPr 365
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1008 GATTCGGCCCTTTGGAGAGACCCCGTGGGACGCTGGCCGCCAATCC 1057
365 oGLuAspAspGLuValProGLuAspThrGLuHisAspAspProAsnSera 382
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1058 ACCAACTGACATCCGCTGATCCAGAGACCGCGACGCTTACCATC 1107
382 sPProAspTYrTYrAsnAspMetProAlaValILleProValGLuGLuThr 398
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1108 CCCCAGCCACCCGGAACACATGGCGCTGATC..... 1139
399 ThrLYsSerSerAsnAlaValSerMetProILlePheAlaAlaPheValAl 415
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1140 .....GCCGGCGCGGTGGCGGCACTTCCTGGCAGCCCTGTGTCAT 1180
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seq_name: /cgn2_6/ptodata/2/1na/backfiles1.seq:5470718-1
seq_documentation_block:
; Patent No. 5470718
; APPLICANT: O'CALLAGHAN, DENNIS J.
; TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
; D NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/954,417
; FILING DATE: 30-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 561,553
; FILING DATE: 01-AUG-1990
; SEQ ID NO:1:
; LENGTH: 2229
5470718-1

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      Ratio: 0.915      Gaps: 21
Percent Similarity: 48.131      Percent Identity: 23.131

alignment_block:
US-09-994-064-11 x 5470718-1 ..
Align seg 1/1 to: 5470718-1 from: 1 to: 2229

25 CysGLyLYsArGcYsCysSerGLyAlaAlaValPheThrLeuPheTr 41
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702 TGCATGGCAATCGCATCTTGAAGCGTGTGCT.....CTCTGTG 742
41 P-ThrCysValArgILleMetArgGLuHisILeCysPheValArgAsnAla 57
| |||||
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336 AlaGluSerSerGluLysLysAlaProProGluAspSerGluAspAspMe 352
      ::::::::::||::: ||::: :::::::::: ||
1543 .....ACACAAATAAAACAGACCCGAACACAGGCCAGCGACCC 1583
      ::::::::::||::: ||::: :::::::::: ||
352 tGlnAlaGluLaserGlyLysAsnProAla.....AlaLeuProG 366
      ::: ::: ::: ||::: ::: ||:::
1584 CAACCCCAATCAGCCTTTTAAGTGCCAGCATCAACACACTTGTGCCAA 1633
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366 LuAspAspGluValProGluAspThrGluHisAspAspProAsnSerAsp 382
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1634 GACTCGATGAGGTGATGAGGTCAATAG..... 1662
383 ProAspTyrTyrAsnAspMetProAlaValIleProValGluGluThrTh 399
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1663 .....CCCGTACAAAGCCCCCAAA.....AC 1685
399 rLysSerSerAsnAlaValSerMetProIlePheAlaIlePheValAlaC 416
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1686 GCTTAAGAGCAACTCTACGTTGTGGGCATCAGCGTCGTTGGGTATCG 1735
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416 ysaIaValAlaLeuValGlyLeuLeuValTrp 426
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1736 CCGGCTAGTATTGTGGGCGCTCATTTATAC 1767
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Date: Sep 29, 2002 10:29 AM

About: Results were produced by the Gencore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

# Command line parameters:

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-Q/cgn2.1/USPTO.spool/US09994064/runat_27092002-185413.13619/app-query.fasta_1.499
-BB=EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=bloms62 -TRANS=human0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pis -NORM=ext -HEADSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09994064@cgn1.1_4874
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMECUT=120 -WARN_TIMECUT=30
-NO_XLUPY -WAIT -THREADS=1
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## Search information block:

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Query: US-09-994-064-11
Query length: 434
Database: EST: *
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1813.990000
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## Score list:

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gb_estc:BG467526	+	115.00	182.79	0.6187	1
gb_estc:BI405354	+	114.00	179.99	0.8865	1
gb_estc:BG468991	-	114.00	174.95	1.69	1
gb_estc:BI905542	+	113.50	177.43	0.123	1
gb_estc:BI948443	+	113.00	181.79	0.7033	1
gb_estc:BG599972	+	113.00	177.84	1.17	1
gb_estc:BG499479	+	111.50	177.94	1.15	1
gb_estc:BI684767	+	111.50	174.91	1.77	1
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gb_estc:BE412830	+	111.00	171.73	2.56	1
gb_gss:CN506390	-	111.00	171.72	2.36	1
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gb_estc:BE599342	+	110.00	176.35	1.41	1
gb_estc:BE63291	-	110.00	175.47	1.58	1
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gb_gss:AG136530	-	110.00	168.42	3.91	1
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gb_gss:CN5044WA	-	106.00	170.40	3.03	1
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gb_estc:BI877213	+	105.00	166.50	5.00	1
gb_estc:BG131584	+	105.00	165.30	5.83	1
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gb_estc:AV0004829	-	104.00	163.85	7.03	1
gb_estc:BE255977	-	104.00	163.85	7.20	1
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gb_gss:CN50717H	-	104.00	159.82	11.78	1

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seq\_name: gb\_hlc:AK004961

seq\_documentation\_block:

LOCUS AK004961 3012 bp mRNA linear HTC 19-JAN-2002  
DEFINITION Mus musculus adult male liver cDNA, RIKEN full-length enriched  
library, clone:1300010N03;transcription factor UBF, full insert  
sequence.

ACCESSION AK004961  
KEYWORDS AK004961.1 GI:12836541  
SOURCE HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA,  
clone:1300010N03.  
Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

Carinci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## TITLE

Genome Res. 10 (10), 1617-1630 (2000)

## REFERENCE

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carinci, P.,  
Kono, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunoto, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

## TITLE

RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipipillary sequencer

## JOURNAL

## PUBMED

## REFERENCE

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## TITLE

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## REFERENCE

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## PUBMED

## REFERENCE

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## TITLE

Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Atakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bulc, C.,  
Carinci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hara, A.,  
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,  
Hoto, D., Imotani, K., Ishii, Y., Itoh, M., Iwama, M., Katsura, T.,  
Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Nunakaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Queckenbush, J.,  
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,  
Schirml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yamane, I.,  
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and  
Hayashizaki, Y.

Direct Submission  
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),



2171 CTCTTTCAGATGCGCGGAGCTTCTGAGTCCAGCAGTGAAGATGAA 2220  
 369 LuValProgluaSPThrLuHisaspasproasnserseraproasPTyr 385  
 2221 GCGAGATGGGGAT...GAGAAATGATGACGACGACGATGAAGATGAC 2267  
 386 TyrAsnAsp 388  
 2268 GAAGATGAC 2276  
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 LOCUS BG467526 661 bp mRNA linear EST 21-MAR-2001  
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 ACCESSION BG467526  
 VERSION BG467526.1 GI:13418130  
 KEYWORDS EST  
 SOURCE Necator americanus.  
 ORGANISM Necator americanus.  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidae; Ancylostomatidae; Bunostominae; Necator.  
 1 (bases 1 to 661)  
 Blaxter, M.L., Parkinson, J., Whittom, C., Daub, J., Guiliano, D., Hall, N., Quayle, M., and Barrell, B.  
 Edinburgh University/Sanger Centre Nematode EST Project  
 Unpublished (2000)  
 CONTACT: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JF, UK.  
 Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk  
 The library was prepared for Dr. David Pritchard University of Nottingham Sequencing was performed by Claire Whittom ICAFB, Edinburgh  
 PCR Primers  
 FORWARD: SAC  
 BACKWARD: T7PL  
 Plate: 04 row: H column: 04  
 Seq primer: SAC  
 High quality sequence stop: 486.  
 Location/Qualifiers  
 1..661  
 /organism="Necator americanus"  
 /db\_xref="taxon:51031"  
 /clone\_lib="Na\_L3\_04H04"  
 /clone\_lib="Necator americanus (parasitic nematode) L3"  
 /sex="Mixed"  
 /dev\_stage="L3"  
 /note="Vector: pCMV-PCR vector; Site\_1: EcoRI (5' end); Site\_2: XhoI (3' end); Necator americanus is a human hookworm, responsible for debilitating anaemia. The library was constructed by David Pritchard (University of Nottingham, UK) from mRNA from N.americanus L3 stage (Nottingham strain) maintained in hamsters."  
 BASE COUNT 203 a 203 c 142 g 113 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 115.00 Length: 115  
 Ratio: 1.885 Gaps: 5  
 Percent Similarity: 53.043 Percent Identity: 32.174  
 alignment\_block:  
 US-09-994-064-11 x BG467526 ..

Align seq 1/1 to: BG467526 from: 1 to: 661  
 309 SerLapPro.....AsProArgProAspSerValProGluIlePr 323  
 313 TCTCTCTCATCGCAGAACGACGACCTGATCAAGTCTCTCAGAGGCC 362  
 323 oAlaValThrLysLysAlaGluGlyArgThrProAspAlaGluSerSerg 340  
 363 TGCACAAATGAACTACTGCTCTGAGGAATCCGCAAAAGTAACTCTTAC 412  
 340 LuLysLysAlaProProGluAspSer...GluAspAspMetGluAlaGlu 355  
 413 AGGAAGCAGCTCCCTCAAAATGCGCTATCAGAAGATGCTCCAGCTGAA 462  
 356 AlaSerGlyGluAsnPro..... 361  
 463 GCTCTCAGAAAGCCGACGATACAGGCTGAACACACAGATGCTCCGATC 512  
 362 .....AlaAlaLeuProGluAspAspGluValProGluAspThrG 375  
 513 CTTGACCACTGCCGAGCACCCTACCGAC.....GCAGAAACTACAC 553  
 375 LuHisaspasproasnserseraproasPTyrTyraAspmetProAla 391  
 554 CACAC.....CCAGATCTGCTCCAGCTCAGAAACTCTCTGCTGCC 597  
 392 ValLeuProValGluGluThrThrLysSerSerAsnAlaValSer 406  
 598 GAGATTACACAGAGACCCGACGTCGTAACCTCACCACATCA 642  
 seq\_name: gb\_est2:BI405354  
 seq\_documentation\_block:  
 LOCUS BI405354 727 bp mRNA linear EST 14-AUG-2001  
 DEFINITION 117B12 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA sequence.  
 ACCESSION BI405354  
 VERSION BI405354.1 GI:15184768  
 KEYWORDS EST.  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 727)  
 Nielsen, K.L., Crookshanks, M., Emmersen, J., and Welinder, K.G.  
 EST-sequencing of mature potato tuber (Var. Kurasa)  
 Unpublished (2000)  
 CONTACT: Karen G. Welinder  
 Institut for Biotechnologi  
 Aalborg Universitet  
 Sohngaardsboeslvej 49, 9000 Aalborg, Denmark  
 Tel: +45 96358467  
 Fax: +45 98141808  
 Email: kwe@bio.auc.dk  
 Sequenced from the 5' end.  
 High quality sequence stop: 727  
 POLYA-No.  
 Location/Qualifiers  
 1..727  
 /organism="Solanum tuberosum"  
 /cultivar="Fleld grown Kurasa"  
 /db\_xref="taxon:4113"  
 /clone\_lib="Mature tuber lambda ZAP"  
 /tissue\_type="tuber"  
 /note="Vector: lambda ZAP"  
 BASE COUNT 238 a 127 c 198 g 164 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 114.00 Length: 268  
 Ratio: 0.927 Gaps: 10

Percent Similarity: 45.896 Percent Identity: 22.761

Alignment\_block:

US-09-994-064-11 x B1405354

Align seg 1/1 to: B1405354 from: 1 to: 727

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134 SerialAlaLysGluLysGluLysGlyProPheGlnAlaSerValVa 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 TCTGCTTCATCGAGCGAGCATCTGATTTTCGGGATCGCGCTAGTCTC... 138
150 LrrpPheTyrValLleLysGlyAspAspGlyLysAspLysTyrCysProI 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 .....TGTGTAA 145
167 LetyrArgLysGluTyrArgGluCysGlyAspValGlnLeuLeuSerGlu 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
146 TGTGA.....CCGTACCGTACTGATGAGACACAGAGAGGCTCAGTCA 189
184 CysAlaValGlnSerAlaGlnMetTrrpAlaValAspTyrValProSerT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 TGTTCGCATGATTAGACAGAGTATG..... 214
200 hrLeuValSerArgAsnGlyAlaGlyLeuThrLlePheSerProThrAla 216
215 .....CTA 217
217 AlaLeuSerGlyGlnTyrLeuLeuThrLeuLysLleGlyArgPheAlaG 233
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
218 ACTTGGCCGCGTCATCCTACTGATGCTTTATTTTCTTCGGTGGTTAA 267
223 nrrAlaLeuValThrLeuGluValAsnAspArgCysLeuLysLleGlyS 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
268 AACTCGAGATCTCCTCCTC.....ACCCAGG 293
250 ergLLeuAsnLeuPheLeuProSerLysCysTrrpThrThrGlnTyrGln 266
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
294 TGTACTGTAAGCTACTCGACAAAGGCTAAAGGGCTGGAAGAACATCAT 343
267 ThrGlyPheGlnGlyGlnHisLeuTyrProLleAlaSerPheAsn...Th 282
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 ATATCTTCCCAAGCAACCTCTTGATGCCGAAGAACACCGCAATGAGAC 393
282 rArgHisAlaAspAspValTyrArgGlyTyrGluAspLleLeuGlnArgT 299
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
394 GGGGATGATGATGATGATGATGAAGTGAAGACTGTCTCATCCGAGATG 443
299 rPAsnAsnLeuLeuArgLysLysAsnProSerAlaProAspProArgPro 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
444 GAGCAATATGTG.....AACATTAACCCAAACACCAATGATAGCAACTCC 487
316 AspSerValProGlnGluLleProAlaValThrLysLysAlaGluGlyAr 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
488 AAGAAACATCTTAGAAN.....GAGCGACGCGTGC 519
332 g..... 332
520 TGAAGAGATGTTGAGATGATGATGATGATGATGATGATGATGATGATG 569
333 ..ThrProAspAlaGluSerSerGlyLysLysAlaProProGluAspSer 348
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
570 ACACTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 610
349 GluAspAspMetGlnAlaGluAlaSerGlyLysAsnProAlaAlaLeuPr 365
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
611 GATATGTGACGAAGATGACCTGATGAAGGCGAGAAAGTACTGTGGAGA 660
365 oGluAspAspLysValProGluAspThrGlnHisAspAspProAsnSerA 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
661 AGAGGACATGATGAAGAGAAAGAAAGAAAGATGATGATGATGATGATG 710
382 sp 382
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711 AA 712

seq\_name: gb\_est2:BG468291

seq\_documentation\_block:

LOCUS

BG468291 1132 bp mRNA linear EST 21-MAR-2001

DEFINITION

602509889F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:464399 5',

ACCESSION

BG468291

VERSION

GI:13400561

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1132)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LCM1415 row: a column: 24  
High quality sequence stop: 528.

FEATURES

Location/Qualifiers

source

1..1132

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:464399"

/clone\_id="NIH\_MGC\_15"

/tissue\_type="adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pORF; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(3). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT

400 a 314 c 268 g 150 t

ORIGIN

1..1132

alignment\_scores:

Quality: 114.00 Length: 356

Ratio: 0.750 Gaps: 17

Percent Similarity: 42.697 Percent Identity: 23.034

alignment\_block:

US-09-994-064-11 x BG468291/rev ..

Align seg 1/1 to reverse of: BG468291 from: 1 to: 1132

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25 CysGlyLysArgCysCysSerGlyAlaAlaValPheThrLeuPheTr 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
812 TGTCTCCCTTTGTTTCTGTTCTGCGCTGCTGCTGCTGCTGCTGCTG 763
41 P..... 41
762 GGGTTTGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 713
42 .....ThrCysValArgLleMetArgGlnHisLleCysPheVal 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
712 TGTCTGATGATGTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
55 ArgAsnLleMetAspArgHisLeuPheLeuArgAsnLlePheTrpThrI 71
::

```



```

296 .. LeuGlnArgTrpAsnAsnLeuArgLysLysAsnProSerAla... 310
      ::::::::::: ||| |||::: |||:::
322 CTTACTAGTCAGCCGTGAATTCTACCCGGGAAACTCCACCAAGAA 371
      ::::::::::: ||| |||::: |||:::
331 ..:::::::::..ProAspProArgProAspSerValProGlnG1 321
      ::::::::::: ||| |||::: |||:::
372 CTGCTGAAGGGGAGAGAGAAACCAAGACAGATGAGTTCAGAGGA 421
      ::::::::::: ||| |||::: |||:::
321 uilleProAlaValThrLysLysAlaGluArgTrpProAspAlaGlu 338
      ::::::::::: ||| |||::: ||| |||
422 ATCTATCTACTGTGTGAAGACAGAGAAATGAGACTCCACCTGCTACAT 471
      ::::::::::: ||| |||::: ||| |||
338 erSerGluLysLysAlaPro.....ProGluAspSerGluAspAsp 351
      ::::::::::: ||| |||::: ||| |||
472 CCAAGTAGGAGAGAGAGCCCAAGGGGAGGCTGAGAGTGAAGAAAGAA 521
      ::::::::::: ||| |||::: ||| |||
352 MetGlnAlaGluAlaSerGlyLysProAlaAlaLeuProGluAspAs 368
      ::::::::::: ||| |||::: ||| |||
522 GAGAACAAACAGCAAGTCTCTGAGAAACCAAAAGAGTGAAGAGATCA 571
      ::::::::::: ||| |||::: ||| |||
368 p.....GluValProGluAspThrGluHisAspAsp..... 378
      ::::::::::: ||| |||::: ||| |||
572 GTCTAAAGAAAAGAGAGAAAGTGAAGATTCCTGCTGGCG 621
      ::::::::::: ||| |||::: ||| |||
379 ..:::::::::..ProAsnSerAspProAspTyrTrpAsnAspMetPro 390
      ::::::::::: ||| |||::: ||| |||
622 ACTCTCTCTCCAGCCAGCTACGCCAGCCAGAGACAAACCCCATG... 668
      ::::::::::: ||| |||::: ||| |||
391 AlaValIleProValGluGluThrThrLysSerSerAsnAlaValSerMe 407
      ::::::::::: ||| |||::: ||| |||
669 GCCTCTCTCTCC.....ACGGCCAAAGATGAGCCCAATCTTAACCTGA 709
      ::::::::::: ||| |||::: ||| |||
407 tProIlePheAlaAlaPheValAlaCysAlaValAlaLeuValGlyLeu 424
      ::::::::::: ||| |||::: ||| |||
710 GGCCTTAAGCAAGCTTCTCCAGAAAGATGGCGCTCGGTGCTGCGATTTC 759
      ::::::::::: ||| |||::: ||| |||
424 euValTrpSerIleValLys 430
      ::::::::::: ||| |||::: ||| |||
760 GAAAGTACATCATTCATTAAG 779
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seq_name: gb_est2:BI948443

seq_documentation_block:
LOCUS BI948443 533 bp mRNA linear EST 19-OCT-2001
DEFINITION HVSMEL0009J10f Hordeum vulgare spike EST library HVCDA0012
(Fusarium infected) Hordeum vulgare cDNA clone HVSMEL0009J10f, mRNA
sequence.
ACCESSION BI948443
VERSION BI948443.1 GI:16288851
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
Pooideae;
Triliceae; Hordeum.
1 (bases 1 to 533)
Wing,R., Muehlbauer,G.J., Close,T.J., Kleinbofs,A., Wise,R., Heinlen
S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J.J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bp bases = 123
Seq primer: AATTAACTCTCACTAAGG
High quality sequence start: 2

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```

FEATURES
    source
        High quality sequence stop: 520.
        Location/Qualifiers
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                /organism="Hordeum vulgare"
                /cultivar="Morex"
                /db_xref="taxon:4513"
                /clone="HVSMEL0009J10f"
                /clone_11b="Hordeum vulgare spike EST library HVCDA0012
                (Fusarium infected)"
                /tissue_type="Spike"
                /lab_host="TJC121"
                /note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
                XhoI; Plants were grown at the University of Minnesota in
                the GJ Muehlbauer lab; spikes were harvested and snap
                frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium
                graminearum inoculation (Heinen). In the TJ Close lab at
                the University of California, Riverside, total RNA was
                prepared from each sample pool, equal quantities of all
                eight RNA pools were combined, poly(A) RNA was purified
                from the mixture, one primary unamplified cDNA library was
                made, and 1 million pfu were in vivo excised to give
                pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi
                ). Phagemids were plated and picked at the Clemson
                University Genomics Institute (CUGI) (Begum, Palmer,
                Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                sequencing and sequence analysis were performed at CUGI
                (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                The sequence has been trimmed to remove vector sequence
                and contains a minimum of 100 bases of phred value 20 or
                above. For more details on library preparation and
                sequence analysis see
                http://www.genome.clemson.edu/projects/barley. To order
                this clone see http://www.genome.clemson.edu/orders Also
                see Close TJ, Wing R, Kleinbofs A, Wise R (2001)
                Genetically and physically anchored EST resources for
                barley genomics. Barley Genetics Newsletter 31:29-30.
                (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT      183 a      141 c      160 g      49 t
ORIGIN
alignment_scores:
    Quality: 113.00      Length: 111
    Ratio: 1.852      Gaps: 4
    Percent Similarity: 54.955      Percent Identity: 28.829
alignment_block:
US-09-994-064-11 x BI948443 ..
Align seq 1/1 to: BI948443 from: 1 to: 533
305 LysLysAsnProSerAlaProAspProArgProAspSerVal...ProG1 320
      ::::::::::: ||| ||| ||| ||| ||| ::
29 GAAAGAGAGCGCTGAGTGTGACGACAAAGGCCCATAGGTAAAGAAAGA 78
      ::::::::::: ||| ||| ||| ||| |||
320 ngUilleProAlaValThrLysLysAlaGluArgTrpProAspAla. 336
      ::::::::::: ||| ||| ||| ||| |||
79 AGAAGAGGATGCCCGCGCAAAAAGAGCCAGAGCAAGAGCCCATCCA 128
      ::::::::::: ||| ||| ||| ||| |||
337 ..:::::::::..GluSerSerGluLysLysAlaPro 344
      ::::::::::: ||| ||| ||| ||| |||
129 GCAACAAATGCCGAGAGAGCCCAAGAGAAAGAAAGAAACACCA 178
      ::::::::::: ||| ||| ||| ||| |||
345 Pro.....GluAspSerGluAs 350
      ::::::::::: ||| ||| ||| ||| |||
179 CCTGTCAAGCAGAGAGAGAGAGAGTCCGAGTCCGAAGTGTAGCA 228
      ::::::::::: ||| ||| ||| ||| |||
350 pAspMetGlnAlaGluAlaSerGlyLysProAlaAlaLeuProGluA 367
      ::::::::::: ||| ||| ||| ||| |||
229 CGACTTGTATTCGAGAGAGAGACTCA.....GAGG 257
      ::::::::::: ||| ||| ||| ||| |||
367 sPAspGluValProGluAspThrGluHisAspAspProAsnSerAspPro 383
      ::::::::::: ||| ||| ||| ||| |||

```







```

285 CTATACGTGAGCCGTGAATTCTACCCGGAAACTCCACCCAAAAGCAAA 334
311 .....ProaspProargProaspServalProglngl 321
335 CTTCGTGAAGGAGAGAGAAAAACCAACACAGATGAAAGTTGAGAGGA 384
321 uileproalaValThrLysLysAlaGluGlyArgThrProaspAlaGlu 338
385 ATCTATCTCTACTGTAGAAGACGAGAGATGACCTCCACCTGCTACAT 434
338 eSerGluLysLysAlaPro.....ProgluAspSerGluAsp 351
435 CCAGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 484
352 MetGlnAlaGluAlaSerGlyLysProAlaAlaLeuProgluAsp 368
485 GAGAAACAGACAACTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGCA 534
368 P.....GluValProGluAspThrGluHisAsp 378
535 GTCTAAAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 584
379 .....ProaspSerAspProaspPtyr 385
585 ACTCTCTGTGCAGACAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 634
386 Tyr.....AsnAspMetProAlaValIleProValGluGluThrTh 399
635 TTCCCTCCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
399 LysSerSerAsnAlaValSerMetProIlePheAlaAlaPheValAla 416
670 TGAGGCCCTTAAGAGATCTTCAGAGAGAGAGAGAGAGAGAGAGAG 719
416 ys...AlaValAlaLeuValGlyLeuValTyr 426
720 TCGAAAGTACATCATCTCAATAGTACCTTCTCTG 754

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seq\_name: gb\_est2:BG480929

seq\_documentation\_block: 1499 bp mRNA linear EST 21-MAR-2001  
 LOCUS BG480929 602530078F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4653474 5',  
 DEFINITION mRNA sequence.

ACCESSION BG480929  
 VERSION BG480929.1 GI:13413208  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 1499)  
 NIH-MGC http://mhc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1CM1439 row: 1 column: 19  
 High quality sequence stop: 220.

FEATURES

source

1. 1499  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4653474"  
 /clone\_lib="NIH\_MGC\_21"  
 /tissue\_type="choriocarcinoma"

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/lab_host="DHI0B (phage-resistant)"
/note=Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G), size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

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BASE COUNT 452 a 387 c 393 g 267 t  
 ORIGIN

alignment\_scores:  
 Quality: 111.50 Length: 369  
 Ratio: 0.697 Gaps: 22  
 Percent Similarity: 43.360 Percent Identity: 23.577

alignment\_block:  
 US-09-994-064-11 x BG480929 ..

Align seg 1/1 to: BG480929 from: 1 to: 1499

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25 CysGlyGlyArgCysCysSerGlyAlaAlaValPheThrLeuPheTr 41
104 TCCTTGGGAGCCAGTGTCTCCGGGGGAGACGCTTTGGGAGCCCTTGT 153
41 PThrCysValArgIleMetArgGluHisIleCysPheValArgAsnAla 58
154 GAGC.....TTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 173
58 eAspArgHisLeuPheLeu...ArgAsnAlaPheThrThrIleValLeu 73
174 TGGAT.....TTCCCTGGGCGGAGGAGATTTCTGCG..... 202
74 LeuSerSerPheAlaSerGlnSerThrAlaAlaValThrTyrAspTyr 90
202 ..... 202
90 eLeuGlyArgArgAlaLeuAspAlaLeuThrIleProAlaValGlyPro 107
203 ...GGCAGAAACCTTGTGGGCTCTGGGAGC.....CCTT 233
107 yAsnArgTyrLeuThrArgValSerArgGlyCysAspValVal..... 121
234 TAAAC.....TCCGGGGGGGTAGATCTTATGTGCTC 265
122 ...GluLeuAsnProIleSerAsnValAspMetIleSerAlaAlaVal 137
266 TGAGAACTTATAGCATGCGAGCAGCAGCCAGCAGCAGCAGCAGCAAG 315
137 sGluLys.....GluLysGlyGlyProPheGluAlaSerValValTyrP 152
316 AGAGAAAGCAGCCGAGAGAGAAATACCTTTAGATCCCGAGGTGCTTT 365
152 heTyrValIleLysGlyAspAspGlyGluAspLysTyrCysProIleTyr 168
366 GTTGGGAGAAAGAGCCCTTACTCAGAGAAAGCGCTTTTGGAAAGCTT 415
168 rArgLys...GluTyrArgGluCysGlyAspValGlnLeuLeuSerGlu 184
416 TCATTAACCTCTCATACCGTAGA.....ATAAATACCT 447
184 yAlaValGlnSerAlaGlnMetTrpAlaValAspTyrValProSerThr 200
448 GTACCTCAATTAATTC.....TATGGCCCTTACGAA 479
201 LeuValSerArgAsnGly.....AlaGlyLeuThrIlePhePhe 213
480 TAAATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 529
213 rProThrAlaAlaLeuSerGlyGlnTyrLeuLeuThrLeuLysIleGly 230

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/organism="Horddeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HM02D15r"
/clone_lib="Horddeum vulgare Barke roots"
/clone_type="roots"

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/!db_host="XLOLR"
/!db_vector="plasmid pBK-CMV, Site_1: EcoRI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were growing
for two days on filter paper at room temperature. Cloning
sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most
cases the EcoRI site is NOT present, as well as the EcoRV
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp"
BASE COUNT      212 a      142 c      192 g      152 t      2 others
ORIGIN

alignment_scores:
      Quality: 111.00      Length: 283
      Ratio: 0.888      Gaps: 13
Percent Similarity: 44.170      Percent Identity: 22.615

alignment_block:
US-09-994-064-11 x AL503461 ..

Align seg 1/1 to: AL503461 from: 1 to: 700

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167 eTyArgLysGlyTyrArgLysCysGlyAspAlaIleLeuSerGlu 183
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184 CysAlaValGlnSerAlaGlnMet.....TTPAl 193
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113 TGGCTGCAAAAGATGGACAGAAAGAGTCCGGCTCTTGACGAATTGGTG 162
193 aValAspTyrValProSerThrLeuValSerAlaGlnGlyLeuT 210
163 T..... 163
210 hrIlePheSerProThrAlaAlaLeuSerGlyGlyTyrLeuThrLeu 226
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164 .....ACTGCATCCGCAGCTTTAGAGAGCGTCGATTCGTGGTACC 205
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260 rThrThrGlnGluTyrGlnThrGlyPheGlnGlyLysIleThrPro 276
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275 GGGTAATGAGAAAAAGCAGAG..... 297
277 IleAlaIlePThrAsnThrArgHisIleAspAspValTyrAlaGlyTyrG1 293
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298 ...CAAGATGCTCTACCGAAGCATCTTAATCCTCTCTCTT...GTTC 341
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310 laProAspProArgProAspSerValProGlnGluIlePro...AlaVal 325
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542 ACCAA.....ATGACACCCGAT 558
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376 HisaspProAsnSerasProaspTyTYrAsnaspMetProAlava 392
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seq\_name: gb\_est2:BE412830

seq\_documentation\_block:

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CDNA clone MCG008.B08, mRNA sequence.  
ACCESSION BE412830  
VERSION BE412830.1 GI:9410578  
KEYWORDS EST.  
SOURCE barley.  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticeae; Hordeum.  
1 (bases 1 to 954)  
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier  
, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,  
Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,  
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,  
Pecchioli, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
Sorrells, M., Warburton, M. and Wenzel, G.  
International Triticeae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticeae  
Unpublished (2000)  
Contact: Graner A  
Institute for Plant Genetics & Crop Plant Research  
Corrensstr. 3, D-06466 Gatersleben GERMANY  
Tel: 49 39482 5137  
Fax: 49 39482 5137  
Email: a-graner@ipk-gatersleben.de  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.

FEATURES  
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/tissue\_type="leaf/culm"  
/dev\_stage="etiolated"

BASE COUNT 266 a 192 c 259 g 227 t 10 others  
ORIGIN

alignment\_scores:  
Quality: 111.00 Length: 283  
Ratio: 0.888 Gaps: 13  
Percent Similarity: 44.170 Percent Identity: 22.615

alignment\_block:  
US-09-994-064-11 x BE412830 ..

Align seg 1/1 to: BE412830 from: 1 to: 954

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|||||
25 TGCTGTAT.....GAGATGGCGAGAGATGAGACTTAGAGGACT 62
|||||
167 eTYrArGlygluTYrArGlyGlycys.GlyAspValGlnleuSerglu 183
|||:
63 CTATGTTCGCAAAACTGAAAGACTGAAAGCTTGGCGGCTCTATCGAAA 112
|||||
184 CysAlaValGlnSeraLaglnMet.....TrpAl 193
|||||
113 TCGGTACAAAGAGTGGACAGAAAGAGTCCGGCTCTGACCAATGTGG 162
|||||
193 aValAspTYrValProSerThrleuValserArgasnGlyAlaGlyLeuT 210
|||
163 T..... 163
210 hrIlePheSerProThrAlaAlaLeuSerglyGlnTyreuleuThrleu 226
|||:
164 .....ACTGCATCCGCAATTTTAGAGAGGCTGATTTGCTGTGAC 205
|||||
227 LysIleGlyArgPheAlaGlnThrAlaLeuValThrleuGluValAsnAs 243
|||
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234 GAAG...CAAAAGCTGTTAATGAGTGTGCG.....GATGACAGAGACT 274
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559 AAGAGTGAATCT.....TCCACAGCATAGAGGTGTGCA 570
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seq\_name: gb\_gss:CNS06X9U  
seq\_documentation\_block:





